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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 03:19:15 ; Search time 2034.91 Seconds
(without alignments)
15518.202 Million cell updates/sec ;

Title: US-09-623-304A-2

Perfect score: 1509

Sequence: 1 ttactactacaacacacc.....tttctctgtccgaattc 1509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*
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33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1436.6	95.2	1856	9	AF153817	AF153817 Homo sapi
3	1436.6	95.2	2089	9	AF153815	AF153815 Homo sapi
4	1436.6	95.2	3642	9	AF153809S6	AF153809S6 Homo sapi
5	1436.6	95.2	4021	9	AF153816	AF153816 Homo sapi
6	1436.6	95.2	12311	9	AC005208	AC005208 Homo sapi
7	1214.4	80.5	1257	9	AF179393	AF179393 Homo sapi
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10	892	59.1	1257	10	AB016197	AB016197 Mus muscu
11	870.6	57.7	1260	10	AF249676	AF249676 Rattus no
12	861.6	57.1	187774	2	AC025586	AC025586 Mus muscu
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33	295.6	19.6	2123	5	GG020216	U20216 Gallus gall
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35	285.6	18.9	1284	4	AF277647	AF277647 Canis fam
36	280.4	18.6	1287	10	AF021136	AF021136 Mus muscu
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38	280.4	18.6	2310	6	I66390	I66390 Sequence 1
39	280.4	18.6	2311	6	I17652	I17652 Sequence 1
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41	272.4	18.1	1284	10	AF021137	AF021137 Rattus no
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 42 from Patent WO0146258.
ACCESSION AX179754
VERSION AX179754.1 GI:15132118
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1730)
Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Yang, J., Reddy, R.,
Gandhi, A.R., Yang, Y.T., and Khan, F.A.
TITLE: Transposers and ion channels
JOURNAL: Patent: WO 0146258-A 42 28 - JUN-2001;
Incyte Genomics, Inc. (US)
FEATURES
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1.1730
Location/Qualifiers
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/db_xref="taxon:9606"
/note="Incyte ID No: 1254635CB1"

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Best Local Similarity 98.7%; Freq. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

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Qy 1501 ccggaatt 1508
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RESULT 2

AF153817

1856 bp

mRNA

linear

PRI 16-MAR-2001

LOCUS

AF153817

Homo sapiens clone 3 inwardly-rectifying potassium channel Kir5.1

DEFINITION

(KCNJ16) mRNA, complete cds.

ACCESSION

AF153817

VERSION

AF153817.1

GI:8132294

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1856)

AUTHORS

Derst, C., Karschin, C., Wismeyer, E., Hirsch, J.R., Preissig-Muller, R., Rajan, S., Engel, H., Grzeschik, K., Daut, J. and Karschin, A.

TITLE

Genetic and functional linkage of Kir5.1 and Kir2.1 channel subunits

JOURNAL

FEBS Lett. 491 (3), 305-311 (2001)

PUBMED

11240146

REFERENCE

2 (bases 1 to 1856)

AUTHORS

Derst, C.

TITLE

Direct Submission

JOURNAL

Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology, Deutschausstr. 2, Marburg 35037, Germany

FEATURES

Location/Qualifiers

SOURCE

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Best Local Similarity 98.7%; Pred. No. 0;
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DB 1708 CGCCAAAT 1715
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LOCUS AF153815
DEFINITION Homo sapiens clone 1 inwardly-rectifying potassium channel Kir5.1
ACCESSION AF153815
VERSION AF153815.1 GI:8132290
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (Bases 1 to 2089)
Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
Preisig,Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and

TITLE	Genetic and functional linkage of Kir5.1 and Kir2.1 channel
JOURNAL	FEBS Lett. 491 (3), 305-311 (2001)
REFERENCE	11240146
AUTHORS	2 (bases 1 to 2089)
JOURNAL	Direct Submission
TITLE	Submitted (25-MAY-1999) Phillips University, Inst. f. Physiology, Deutschlandstr. 2, Marburg 35037, Germany
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Best Local Similarity	98.7% Pred. No. 0;
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LOCUS AF153809S6 3642 bp DNA linear PRI 16-MAR-2001

DEFINITION Homo sapiens inwardly-rectifying potassium channel Kirs.1 (KCNJ16)

ACCESSION AF153814

VERSION AF153814.1 GI:8132310

KEYWORDS 6 of 6

SEGMENT human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3642)

AUTHORS Dersl.C., Karschln.C., Wischmeyer.E., Hirsch.J.R., Preislg.Muller.R., Rajan.S., Engel.H., Grzeschik.K., Daut.J. and Karschln.A.

TITLE Genetic and functional linkage of Kirs.1 and Kir2.1 channel subunits

JOURNAL FEBS Lett. 491 (3), 305-311 (2001)

PUBMED 11240146

REFERENCE 2 (bases 1 to 3642)

AUTHORS Dersl.C.

TITLE Direct Submission

JOURNAL Submitted (25-MAY-1999) Philipps University, Inst. f. Physiology, Deutschausstr. 2, Marburg 35037, Germany

FEATURES

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Query Match	Best Local Similarity	98.7%	Score 1436.6	DB 9	Length 4021	
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Db 562	ATAGCTGGAAGAGAGAGCAAGCAAGAGATTTACTTCAAAAGATGGCAGCTGTAATGTC	621				
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QY 241	gtgacacccaagtggcgccatatgttttgatatttcttatacttatactctcgtg	300				
Db 682	GTGGACACCAAGTGGCGGCATATGTTTGATATTTCTTATCTTATATTCCTCTGTCGG	741				
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DEFINITION
Homo sapiens inward rectifier potassium channel Kir5.1 (KCNJ16)
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VERSION
AF179353.1
KEYWORDS
AF179353.1 GI:9957531
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1257)
Li, Y., McKenna, E., Figueroa, D. J., Blevins, R., Austin, C. P.,
Bennett, P. B. and Swanson, R.
The human inward rectifier K+ channel subunit Kir5.1 maps to
chromosome 17q25 and is expressed in kidney and pancreas
Unpublished
TITLE
2 (bases 1 to 1257)
REFERENCE
Li, Y. and McKenna, E.
Direct Submission
AUTHORS
Submitted (20-AUG-1999) Bioinformatics, Merck & Co., Inc.,
JOURNAL
WP42-300, West Point, PA 19486, USA
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gland"
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Best Local Similarity 99.2%; Pred. No. 5.2e-313;
Matches 1249; Conservative 2; Mismatches 4; Indels 4; Gaps 3;
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Qy 106 ccgccaagacacattatagctgagaagaagaagaagaagcgaattacttacaagaat 165
Db 61 CCGCCAGACACATTTATACCTGAGAGAGACAGCAAGACGATTTACTTACAAAGAT 120
Qy 166 ggcagctgtaatgtctacttcaagacacatttttggagaatggggaagctatgtgtgac 225
Db 121 GCGAGCTGTAATGTCTACTTCAAGCAGCATTTTGGAGATGGGAAGCTATGTGTTGAC 180
Qy 226 atcttcacacctctgttgaacccaagtggtgcacatgtttgtgatatcttcttacct 285
Db 181 ATCTTACACACCTCTGTGACACCAAGTGGCCGCAATGTGTGTATTTCTTATCT 240

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Oy 286 tatactctcgtgtgataatggtctctgtcttcttgatagccttcatcatgagc 345
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Db 301 GATCTATTAAAGATCCAGACATCACCTTGTGTGACAAAGCTCCATTCCTTTCACAGG 360
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Db 361 GCGTTTGTCTCTCCCTAGAGACCCAAACACATAGATAGTTATGCTGTACT 420
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Db 721 GTCAAGACCAATATCATCTGCTGTCACCCGATACATGTGTCATGAATGACCATGAG 780
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Oy 1246 accctatcagaagactctccctgactttaaangaaatcctctgtgtgaaatcccaatgt 1304
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RESULT 8
LOCUS AL662912 194041 bp DNA linear HTG 31-JAN-2002
DEFINITION Mus musculus chromosome 11 clone RP23-408D5, *** SEQUENCING IN

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PROGRESS **, in unordered pieces.
ACCESSION AL662912
VERSION AL662912.10 GI:18477421
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVIFIER; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Tracey, A.
AUTHORS 1 (sites)
TITLE Direct Submission
JOURNAL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18476962.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM408D5
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 193498 bases at least Q40
Consensus quality: 193567 bases at least Q30
Consensus quality: 193654 bases at least Q20
Insert size: 193741; sum-of-contrigs
Insert size: 190800; 1.9% error; agarose-fp
Quality coverage: 10.92x in Q20 bases; sum-of-contrigs Quality
coverage: 11.24x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Matches 1167; Conservative 2; Mismatches 277; Indels 37; Gaps 5;
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Db 76956 CCTTAAGAGACCAAGAAATGAGCTATTACGAAAGTACAGATCGTCAATGTGG 77015
Oy 86 acgcaataatccagagctaccgagcagacatataatgctgagagaagaagagcaaga 145

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Dp	77016	ACTCCAAATATATCCAGGCTATCTCTCCAGAGCAATGCCATGCTAGAAAGAAAGACAGAGA	77015
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Dp	77136	GGGGAGCTACATGGTTGATATTTTACCACCTTGTGGATATCCAAATGGCCCATATGT	77195
Oy	266	ttgtgataltttcttattactatattctctcgtgtgtgatatattggtctgtcttttgc	325
Dp	77196	TGCTAATATTTTCTCTGTCTTCATTCTCTCTGGTTGATATTTTGGCTTCATATTTTGGC	77255
Oy	326	tcaatgaccttcaatcatalgycgactatcatttaaatgataccagaacacacactgtgtga	385
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Oy	506	ccatttcaatgtcatalcataaataacattatcatttggagctgcctgtggccaatgtgcaa	565
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Dp	77556	ACGGGAACCTTGCTCCTCATGTGGCCATATAGTGACTTCCGACCAACATGTGTGAGAG	77615
Oy	686	gaacagttagagcccaacttctcgtatacagaagaagatgaaggagatgacatg	745
Dp	77616	GCACGCTAGAGACCCACACTTGTGCCCTTTTCAGAAAGACGTGAAGAGAGATGACAGATGG	77675
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Oy	806	tccatgaaattgacacatgagagccctctgtlatgtcccttgcacgcgcaaaagcagtagc	865
Dp	77736	TCCATGAATATGACCATATGAGAGCCCTCTGTATGTGCCCTTGACCGCAAGGACAGTGC	77795
Oy	866	ataactttgagatlttgttgnacattactatctactcgtgtgatttccacttgaacatctacc	925
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Dp	77856	AGTCAGAAATTTCCATACATCCCCACAGAAATTTCTGTGGGCCACAGCTTTCATATGTAT	77915
Oy	986	tggaaagttaagaagagaatataacaaagtgaactgtcactcaglttgaaggagttgtgaag	1045
Dp	77916	TGGAAAGTAAAGAGAAAGTACATCAAGGTGAACGTCTTCAGTTTGAAGAGCGTGGAG	77975
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Dp	77976	TCTACGCCCTTTTGCAGTGCACAACACATGTGATGGAAAGACCAACTCAACAACCT	78035
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Dp	78096	CTTATAGGCGAGTTCCTCTGTGTGACCACTTGTGAAACCCAGAGAGACCGTCTGTGCC	78154

OY	1223	gcacacatgaataaaggaaacacccttaacgaagcctccgaacttaacangaa	1282
Db	78155	CCACAAGTGAATGTAAAGAGATGCCCTATACGAAGAGCCCT-CTGACCTTTAAATAGAT	78213
OY	1283	tcctctgtwgaaatcccaaatgttagtcctaaaatgtcaatlaagsygtaccactgaat	1342
Db	78214	CTCCATGGAGATCCCGAATGTACCCCTCTCTCCGACCCCTATCTAAGG-----	78262
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Db	78263	-----CCGAAAGCTGTAAAGCATGTTTAAACAAAGGTTTAGTTC	78302
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RESULT	9	
AL592422		
LOCUS	AL592422	205947 bp DNA linear HTG 06-DEC-2001
DEFINITION	Mus musculus chromosome 11 clone RP23-218016, *** SEQUENCING IN	
PROGRESS	***, in unordered pieces.	
ACCESSION	AL592422	
VERSION	AL592422.10	GI:17426517
KEYWORDS	HTG; HTGS_PHASE1; HTGS_ACTIVATOR; HTGS_DRAFT; HTGS_PULLTOP.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (05-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,

COMMENT

```

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: hunquerry@sanger.ac.uk
-----
Project Information
Center project name: Bm218016
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Summary Statistics
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 205509 bases at least Q40
Consensus quality: 205628 bases at least Q30
Consensus quality: 205703 bases at least Q20
Insert size: 205747; sum-of-contigs
Insert size: 189076; 6.5% error; agarose-fp
quality coverage: 11.16x in Q20 bases; sum-of-contigs quality
coverage: 12.15x in Q20 bases; agarose-fp

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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

Source

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„Plus“

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mosome="11"

e="RP23-218016

2 =

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MISC_1

08844

Accession: 01393

assembly_line

general: 01363

DEFINITION	R. rattus mRNA for inward rectifier 9.
ACCESSION	X83581
VERSION	X83581.1 GI:609671
KEYWORDS	inward rectifier potassium channel.
SOURCE	black rat.
ORGANISM	Rattus rattus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 1155) Bond, C.T., Pessia, M., Xia, X.M., Lagrutta, A., Kavanaugh, M.P. and Adelman, J.P.
TITLE	Cloning and expression of a family of inward rectifier potassium channels
JOURNAL	Recept. Channels 2 (3), 183-191 (1994)
MEDLINE	95179470
REMARK	Erratum: ([published erratum appears in Receptors Channels 1994;2(4):following 350])
REFERENCE	2 (bases 1 to 1155)
AUTHORS	Adelman, J.P.
TITLE	Direct Submission
JOURNAL	Submitted (19-DEC-1994) J.P. Adelman, Vollum Institute for Advanced Biomedical, Research (VIABR), Oregon Health Sciences University, L4/4, 3181 SW Sam Jackson Park Rd., Portland OR 97201, USA
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106	ccgcagagcacatataagctgtgagaagaagaagcagaagcagatctaccacaaagt 165
61	cctccagacacatgacatagccaggaagaagagcagagcagcgccctgccacaaagat 120
166	ggcagcgtgtaatgctctactccaagacatcttttgagaagaatggggaagcctatggtgtac 225
121	ggcagcgtgtaacggtgtacttttaaacacatttttggagaatggggagctacatggtgat 180
226	atctccacacactctgtgagcacaagaatggcgacatctgttgatattcttcatat 285
181	atattccaccacactctgttgatataccaagtgcccccatattttgtatattttctttgtct 240
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241	tacattctctcctcgttgatattccgctccatatttttggcctcatagacccttcacagga 300

OY	346	gattctattaatgatccagaacatacacacttgltgttgaacaagtcattctttcaagg	405
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OY	406	gccttttgttccctcctaagaaaccaaacaccataagataltgltlcatcgatgttaact	465
Dd	361	GGTTTTTATTTCCTCCTTGAGACCMAACACACATCGGGGTACGGTTACCGTTGGTGCAG	420
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OY	1066	gccaaagcaattgnaacttgtaaaagaccagaagctccca-----tagaaaaagaccacaacg	1121
Dd	1021	GCCAACACACTGTGACTGGAGAAGSCCAACACAGCTCAACAACTTGGAGAAAACGTCCCTTCG	1080
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Dd	1141	GGTGAGCAGCTG 1152	
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LOCUS	AF021138	1284 bp	mRNA linear MAM 07-AUG-2000
DEFINITION	Oryctolagus cuniculus inward rectifier potassium channel (IRK1)		
ACCESSION	AF021138		
VERSION	AF021138.1	GI:2460305	
KEYWORDS	Rabbit.		
ORGANISM	Oryctolagus cuniculus		
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			

REFERENCE 1 (bases 1 to 1284)
 AUTHORS Rae,J.L. and Sheppard,A.R.
 TITLE Inwardly rectifying potassium channels in lens epithelium are from
 the IRK1 (Kir 2.1) family
 JOURNAL Exp. Eye Res. 66 (3), 347-359 (1998)
 MEDLINE 98286410
 PUBMED 9533862
 REFERENCE 2 (bases 1 to 1284)
 AUTHORS Rae,J.L. and Sheppard,A.R.
 TITLE Direct Submission
 JOURNAL Submitted (28-AUG-1997) Physiology and Biophysics, Mayo Foundation,
 200 1st Street SW, Rochester, MN 55905, USA
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Query Match 21.0%; Score 317; DB 4; Length 1284;
 Best Local Similarity 60.7%; Pred. No. 1.3e-73;
 Matches 559; Conservative 1; Mismatches 346; Indels 15; Gaps 2;

QY 142 agaagacgaltactcaagaatgagcagctgtaatgctactcaagcaattttgga 201
 DB 130 AGGAGCGCTTGTGAAGAAAGATGGCCATGCCATCCAGTCAACAGTGGTGAG 189
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 DB 190 AAGGACACAGATACCTTGACAGACATCTTACACAGTGTGGACATTCCTGGCGATGG 249
 QY 262 atgttgtagattttcttatactatctctcgtggtgattggtcgcgtctt 321
 DB 250 ATGTGTTATCTTCTCCCGGCGTTGTCTCTCCCGCATTTTGGCTGTGTTT 309
 QY 322 tggctacatccttcaatcgtgacgtatcttaaatgacacacacacttgctt 381
 DB 310 TGGTGTATACCTCTGCTCCATGGGATCTGATGCTTCTAGAGAGACCAAAAGCCTGTGTG 369
 QY 382 gacaagctcatcttcaagaagggtcttggctccctagaagacaaacacacata 441
 DB 370 TCTGAGGTCAACAGCTTCAACAGCGCTTCTTCTCCATCGAGACCAACACATA 425
 QY 442 ggaatggtatcgcgtgctgctgactgaagaatgctgctggtcgtcgtgctc 503
 DB 430 GGTATGCTTCGGGTGTGTCACAGAGAACGCCAGTGTCTGTTTCATGTGTGTTTC 489
 QY 502 cagttcaatcttaagtgtgacatcaataacttatacttgtagagcttgccctggccaagt 561

DB 490 CAGTCAATCTGGGCTGCATATTCGATGCCCTTATCATTTGGCGCAGTCATGCCAAGATG 549
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 DB 550 GCAAGCCGAAGAGAGAGAAAGAGACCTGTGCTTTCAGTCAATGCTGATGCCATG 609
 QY 622 agaagatggaagcttgctcctatgctgagcagcttggtgattgctgccaacagtgta 681
 DB 610 AGAGATGGCAAGCTGTGCTCATGTGGCGAGTGGCAACCTTGGAAAGACCACTTGGTG 669
 QY 682 gaaggaacagltagagcccaacttcgcgtatacagaagaagtgaaaggaagg--atg 738
 DB 670 GAACCCATGTTGAGCAGCAGCTCTCAATTCAGAAATTAATCTTGAAGGGGAGTATATC 729
 QY 739 agcagtgcatcttaagagccccaatgagtc-----aacgccaatatactcg 786
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 DB 850 AACAGGACATGACATGACAGCTTGAATTTGTGAATTAATGGAAGGACATGGTGAA 909
 QY 907 tcaactggaacatctcccaactcagaagctccctatgttcccgaraatctctgggc 966
 DB 910 GCCACTGCCATGACACACAGATGCCGAGCTCATCTTGGGAAATGCTCTGGGCG 969
 QY 967 catggttcaatgctgctggaagcttaagaaggaagatcacaagtgaaactgcttcaag 1026
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 QY 1027 ttgaaaggaagtgtagaagta 1047
 DB 1030 TTCACACAAACCTATGAAATG 1050

RESULT 15
 LOCUS RABPC 2342 bp mRNA linear MAM 05-FEB-1999
 DEFINITION Rabbit mRNA for potassium channel, complete cds.
 ACCESSION D21057
 VERSION D21057.1 GI:464193
 KEYWORDS K+ channel; potassium channel.
 SOURCE Oryctolagus cuniculus (strain New Zealand white) heart cDNA to
 mRNA, clone RBH1K1.
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 2342)
 AUTHORS Ishii,K.
 TITLE Direct Submission
 JOURNAL Submitted (02-OCT-1993) Kuniaki Ishii, Tohoku University School of
 Medicine, Department of Pharmacology; 2-1 Seiryomachi Aoba-ku,
 Sendai, Miyagi 980, Japan (tel:022-274-1111(ex.2173),
 Fax:022-273-6996)
 REFERENCE 2 (bases 1 to 2342)
 AUTHORS Ishii,K., Yamagishi,T. and Taira,N.
 TITLE Cloning and functional expression of a cardiac inward rectifier K+
 channel
 JOURNAL FEBS Lett. 338 (1), 107-111 (1994)
 MEDLINE 94139886
 COMMENT Submitted (02-Oct-1993) to DBJ by:
 Kuniaki Ishii
 Department of Pharmacology
 Tohoku University School of Medicine
 2-1 Seiryomachi, Aoba-ku
 Sendai, Miyagi 980
 Japan
 Phone: 022-274-1111 x2173
 Fax: 022-273-6996.

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9986"
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BASE COUNT 621 a 526 c 550 g 645 t
ORIGIN

Query Match 21.0%; Score 317; DB 4; Length 2342;
Best Local Similarity 60.7%; Pred. No. 1.3e-73;
Matches 559; Conservative 1; Mismatches 346; Indels 15; Gaps 2;

QY 142 agaaagcgtactctcaaaagatgagcagtgtaatgtctactcaagcacattttgga 201
DB 489 AGGAGCGCGCTTCGTGAAGAGAGATGGCCACTGCAACGTTCATCAACGTGGAG 548
QY 202 gaatgggaaagctatgtgtgacatcttcacacatctgtgagaccaaagtgcgcat 261
DB 549 AAGGACAACAGATACCTTCGACATCTTACCAACGTGTGGACATTCGCTGGCATGG 608
QY 262 atgttgtgataattcttactatctatctctgtgtgtgtatattgagctgtctt 321
DB 609 ATCTGGTATCTTCCTGCGGCTTGTCTCCCTGCTATTTTGGCTGTGCTTT 668
QY 322 tggctatagaccttcaatgacatcttaatgatacagacatcacactgtgtc 381
DB 669 TGGTTGATACCTGCTGCGCATGGGATCTGAGTCTTGAAGAGCAAAAGCTGTGTG 728
QY 382 gacaacgtccatctcttcaacaggagccttltgtctccttagagaccaaaccacata 441
DB 729 TCTGAGGTCAACAGCTTCACAGCGCTTCTTTCATCGAGACCAACACACATA 788
QY 442 agatagtgtatcgtgtgttactgaagaatgtctgtgacgtgtcatgtgtatctc 501
DB 789 GGCATATGGCTTCGCGTGTGTACAGAGCAAGATGCCAGTTGCTTTCATGTGTGTTC 848
QY 502 caatcactcttaagtgacataaataacttatactttagagctgtgtgccaatg 561
DB 849 CAGTCAATCTGGGCTGCAATATGATGCTTATCATTTGGCGCATGCAAGATG 908
QY 562 gcaactgtcgaagaagagcccaaccatcgtttcagctacttgcacttatagtatg 621
DB 909 GCAAGCGCGAAGAGAAAGAGAACGCCCTGTCTTCATGATGATGATGATG 968
QY 622 agagatgggaagcttgcctcatgtgagcattgtgtatattcgggccaacacgtgta 681
DB 969 AGAGATGGCAAGCTGTCTCATGTGCGAGTGGCAACCTTCGGAAGCACTTGTGTG 1028
QY 682 gaaggaacaagttagagcccaacttccgctatacagaagaagcagtgaggag---atg 738
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QY 739 acgatggcattaaagacctcaaatagtc-----aacgaccaatcatcctg 786
DB 1089 CCCCTGGATCAAAATAGACATCATGTGGGTTTGACAGCGGATGTGACCGTATATTCCTG 1148
QY 787 gtaccccggttaactatgttcatgaaattgacatgagagccctctgtatgcccctgac 846

DB 1149 GTGCCCCCATCAAAATAGACAGAAATGATGAGACAGACCCCTTATATGACTTGAGT 1208
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QY 967 cataagtttaatgtcttctggaagttaagaaggaagtattacaagtgaactgtctacag 1026
DB 1329 CACCGCTATGAGCCTGTACTCTTTGAAGAGAGACACTATTACAAAGTGACTATTGAGG 1388
QY 1027 ttgaaggaagtggtggaagta 1047
DB 1389 TTCACAAACCTATGAGTA 1409

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[illegible]

XX Silvia C, Yu W;
PI
XX WPI: 1999-551066/46.
DR
XX P-PSDB: AAY42260.

PT A new potassium channel alpha subunit, Kir5.1, useful for treating
PT hypertension, acute or chronic renal failure, diabetes insipidus or
PT nephropathy -

PS Claim 4: Page 64-65; 68pp; English.

XX This sequence represents a human Kir5.1 inward rectifier potassium
CC channel alpha subunit cDNA. This was isolated and amplified from a human
CC cDNA library using PCR primers AA221042 and AA221043. The Kir5.1
CC alpha subunit is predicted to be approximately 43 kD. The C-terminal
CC tail region (residues 352-383) is divergent with respect to Kir5.1
CC proteins from other species - for example, there is only 10% identity
CC between the Kir5.1 tail regions of human and rat. Potassium channels are
CC typically formed by four alpha subunits, each with two transmembrane
CC domains, and can be homomeric (made of identical subunits) or heteromeric
CC (made of two or more distinct types of alpha subunits). The human Kir5.1
CC alpha subunit associates with additional alpha subunits to form a
CC potassium channel which allows potassium influx to a cell, with little
CC potassium outflux (inward rectifier activity). Such inward rectifier
CC potassium channels comprising human Kir5.1 can be heteromeric, containing
CC one or more Kir5.1 alpha subunits, along with other alpha subunits from
CC the Kir family. Kir5.1 can also comprise a homomeric inward rectifier
CC channel. The cDNA can be used to screen for modulators of inward
CC rectifier potassium channels that contain a Kir5.1 subunit, for the
CC treatment of hypertension, acute or chronic renal failure, diabetes
CC insipidus or diabetic nephropathy, hypo- or hyperthyroidism, gout, etc.
CC hypo- or hyperparathyroidism, pancreatic insufficiency, diabetes, cystic
CC fibrosis, statorrhoea, and salivary insufficiency.

XX Sequence 1509 BP: 435 A; 329 C; 320 G; 422 T; 3 other;

Query Match 99.9%; Score 1507.2; DB 20; Length 1509;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 agcagctatcatatcatcaatcgagacgcaaaataaccagctaccgcccagagacacatt 120
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DB 121 atagctgagaagaagaagcaagaagcattactacaaagaatgagcagctgtaattgc 180
QY 181 tacttcaagcaaatcttggagaatgggaagctatggttgacacttccaccactct 240
DB 181 tacttcaagcaaatcttggagaatgggaagctatggttgacacttccaccactct 240
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DB 241 gggagacacaaatgagcagcatatgttggatattcttcatatatacttcctctg 300
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DB 301 ttgatatattgctctgtcttcttggtcctacagcttcatcatatgagcattatgaatg 360
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QY 421 ctgagagaccac 480
DB 421 ctgagagaccac 480

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QY 1501 ccggaattc 1509
DB 1501 ccggaattc 1509

RESULT 2
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ID AAD09566 standard; cDNA: 1730 BP.
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AC AAD09566;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human transporter and ion channel-15 (TRICH-15) cDNA.
XX
XX Human; transporter and ion channel-15; TRICH-15; cystic fibrosis; mood;
KW gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
KW hypertension; angina; neurological disorder; epilepsy; vaccine; arrhythmia;
KW dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia;
KW Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
KW Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
KW demyelinating disease; mental disorder; Schizophrenia; polymyositis;
KW muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
KW dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
KW scleroderma; pulmonary artery stenosis; nocturnal; Addison's disease;
KW malabsorption syndrome; hypercholesterolaemia; cancer; ss.
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OS Homo sapiens.
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FH Key Location/Qualifiers
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FT mat_peptide 118..1380
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PD 28-JUN-2001.
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XX 22-DEC-2000; 2000WO-US35095.
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XX 23-DEC-1999; 99US-0172000.
PR 14-JAN-2000; 2000US-0176083.
PR 21-JAN-2000; 2000US-0177332.
PR 28-JAN-2000; 2000US-0178572.
PR 02-FEB-2000; 2000US-0179758.
PR 10-FEB-2000; 2000US-0181625.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P,
PI Hillman JL, Azimzal Y, Yue H, Nguyen DB, Yao MG, Gandhi AR,
PI Tang YT, Khan FA;
XX
DR WPI: 2001-418042/44.
DR P-PSDB: AAE04902.
XX
XX Novel human transporter and ion channel proteins useful for treating
PT and preventing transporter, neurological, muscle and immunological
PT disorders
XX
PS Claim 5; Page 150-151; 160pp; English.
XX
XX The present sequence is transporter and ion channel-15 (TRICH-15) cDNA.
CC TRICH is used as vaccine. TRICH is useful for treating a disease or
CC condition associated with decreased expression of functional TRICH,
CC such as transport disorder including amyotrophic lateral sclerosis,
CC cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth
CC disease, Duchenne muscular dystrophy, angina and hypertension,
CC neurological disorders including Alzheimer's disease, amnesia, bipolar
CC disorder, dementia, depression, epilepsy, ischaemic cerebrovascular

CC disease, stroke, cerebral neoplasms, Pick's disease, Huntington's
CC disease and Parkinson's disease, demyelinating diseases, mental disorders
CC including mood, anxiety, Schizophrenia and seasonal affective disorder,
CC muscle disorder including cardiomyopathy, myocarditis, polymyositis,
CC dermatomyositis, arrhythmias and asthma and immunological disorders
CC including AIDS, adult respiratory distress syndrome (ARDS), allergies,
CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
CC syndrome, systemic lupus erythematosus and other diseases including
CC sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
CC artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
CC glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
CC psoriasis and viral, bacterial, fungal, helminthic and protozoal
CC infections. TRICH DNA is useful in gene therapy and in diagnostic
CC purposes.
XX
SQ Sequence 1730 BP: 520 A; 358 C; 361 G; 491 T; 0 other:

Query Match 95.2%; Score 1436.6; DB 22; Length 1730;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

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OY 61 agcagctatcatatcatatcatatcagcagcaaaatccccggctaccgccgaagacatt 120
DB |||||||
DB 142 agcagctatcatatcatatcagcagcagcaaaatccccggctaccgccgaagacatt 201
OY 121 atagctggaagaagaagaagaagaagaacagatcattcacaagaatgagcagctaatgctc 180
DB |||||||
DB 202 atagctggaagaagaagaagaagaagaacagatcattcacaagaatgagcagctaatgctc 261
OY 181 tactccaagcacattttggagaaatgagggaagctatggttgacaattccacactctt 240
DB |||||||
DB 262 tactccaagcacattttggagaaatgagggaagctatggttgacaattccacactctt 321
OY 241 gtgagacacaaatggcgccatagtttgatatttcttcttatacttcttcctg 300
DB |||||||
DB 322 gtgagacacaaatggcgccatagtttgatatttcttcttatacttcttcctg 381
OY 301 ttgatatgtgctcgtctcttgggtcctatagccttccatcagctgagctataatgatt 360
DB |||||||
DB 382 ttgatatgtgctcgtctcttgggtcctatagccttccatcagctgagctataatgatt 441
OY 361 ccagacatcacacttggttgacaagctcattcttcaaggggcctttgtcttc 420
DB |||||||
DB 442 ccagacatcacacttggttgacaagctcattcttcaaggggcctttgtcttc 501
OY 421 ctaggagcccaaacacacatagatagttatgctggttactcgaagaatgattctg 480
DB |||||||
DB 502 ctaggagcccaaacacacatagatagttatgctggttactcgaagaatgattctg 561
OY 481 gccgtgctatggtatcctccagtcacatcctaagttgcatcataatccttcaatt 540
DB |||||||
DB 562 gccgtgctatggtatcctccagtcacatcctaagttgcatcataatccttcaatt 621
OY 541 ggaagctgcttgagcaaaatggcgaactgctgaaagaagacccaacatctgcttcagc 600
DB |||||||
DB 622 ggaagctgcttgagcaaaatggcgaactgctgaaagaagacccaacatctgcttcagc 681
OY 601 tacttgcaattatagatagatagatagatagatagatagatagatagatagatagat 660
DB |||||||
DB 682 tacttgcaattatagatagatagatagatagatagatagatagatagatagatagat 741
OY 661 ttctggccaacacagctggttagaagaacagttagaagccaactctccgcatatacaga 720
DB |||||||
DB 742 ttctggccaacacagctggttagaagaacagttagaagccaactctccgcatatacaga 801
OY 721 gacagtgaaaggagatgacgatgacgatgacgatgacgatgacgatgacgatgacgatg 780
DB |||||||
DB 802 gacagtgaaaggagatgacgatgacgatgacgatgacgatgacgatgacgatgacgatg 861

QY	781	atctctgttcaaccccggttaactatctgtccatgtgaattgaccaaagagccctctgatgccc	840
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QY	841	cttgaccgcgcaaaacagtaagccaaagaataactcttgagattctgtgacattatcatact	900
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QY	1021	ttaacagtttgaaggaagtgctggaagatatactgcccccttttgacgtgcaccaagaattgac	1080
Db	1102	ttaacagtttgaaggaagtgctggaagatatactgcccccttttgacgtgcaccaagaattgac	1161
QY	1081	tgggaagaaccagcagctccacatagaanaagacacacacagtttcgagaatcctgcacgtcg	1140
Db	1162	tgggaagaaccagcagctccacatagaanaagacacacacagtttcgagaatcctgcacgtcg	1221
QY	1141	gacacccaaggcgaagacgaagtgatcttaagtctgacgttgcacagctgtgtgaana	1200
Db	1222	gacacccaaggcgaagacgaagtgatcttaagtctgacgttgcacagctgtgtgaana	1280
QY	1201	ccctcgagagagacacacacactcttcgcacacatgaatatagggaaacacacttatcagaagc	1260
Db	1281	ccctcgagagagacacacacactcttcgcacacatgaatatagggaaacacacttatcagaagc	1340
QY	1261	tctctccgactttaaacangaatccctctgtwaaatcccaaatggtctagtcctcaaatgtga	1320
Db	1341	tctctccgactttaaacangaatccctctgtwaaatcccaaatggtctagtcctcaaatgtga	1395
QY	1321	attatgagggctaacactgtacattatcttccacccaatcaaatgctggtgtgaacgtg	1380
Db	1396	attatgagggctaacactgtacattatcttccacccaatcaaatgctggtgtgaacgtg	1455
QY	1381	gcttttttgaagaagtgtatgctcatgctttatagatgatatgctgtggaatagagtaagta	1440
Db	1456	gcttttttgaagaagtgtatgctcatgctttatagatgatatgctgtggaatagagtaagta	1515
QY	1441	aacttggttaaaagataatctcaaaatccatagttctcagttatcaaatcttctgtgt	1500
Db	1516	aacttggttaaaagataatctcaaaatccatagttctcagttatcaaatcttctgtgt	1575
QY	1501	ccggaatt 1508	
Db	1576	cgcgaatt 1583	
RESULT 3			
AAK05088			
ID	AAK05088 standard; DNA; 1921 BP.		
XX			
AC	AAK05088;		
XX			
DT	05-NOV-2001 (first entry)		
XX			
DE	Human brain expressed single exon probe SEQ ID NO: 5079.		
XX			
KW	Human; brain expressed exon; gene expression analysis; probe;		
KM	microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;		
KW	epilepsy; cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200157275-A2.		
XX			
PD	09-AUG-2001		

XX 30-JAN-2001; 2001WO-US00667.
 PF
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 PI
 XX
 PS Example 4; SEQ ID NO: 5079; 650pp + Sequence Listing; English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 CC
 SQ Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;
 XX

[illegible]


```

QY 541 gtagctgcttggccaaatggcaactgtcgaagaagagcccaaccatcttccagc 600
   |||||
DB 830 ggagctgcttggccaaatggcaactgtcgaagaagagcccaaccatcttccagc 889
QY 601 tacttgcaactatagatgtgagagatgggaagcttgcctcatgtgagcatgtgat 660
   |||||
DB 890 tacttgcaactatagatgtgagagatgggaagcttgcctcatgtgagcatgtgat 949
QY 661 ttctggccaaacagctgtgtagaagaagatggagcccaacttccgctatacagaa 720
   |||||
DB 950 ttctggccaaacagctgtgtagaagaagatggagcccaacttccgctatacagaa 1009
QY 721 gacagtgaaggagatgtagcagatgcatltaaaagacctcaaatagtcacagccaatc 780
   |||||
DB 1010 gacagtgaaggagatgtagcagatgcatltaaaagacctcaaatagtcacagccaatc 1069
QY 781 atcctggttaccctggtaactatgtccatgaaattgacacatgagagccctctgtatgc 840
   |||||
DB 1070 atcctggttaccctggtaactatgtccatgaaattgacacatgagagccctctgtatgc 1129
QY 841 cttagccgcaaaagcagtagcaaaagataacttgagatttggtagcatltaactact 900
   |||||
DB 1130 cttagccgcaaaagcagtagcaaaagataacttgagatttggtagcatltaactact 1189
QY 901 ggtgattccacttgaacatctcacaacatctagaagctcctatgttcccgaraattctc 960
   |||||
DB 1190 ggtgattccacttgaacatctcacaacatctagaagctcctatgttcccgaraattctc 1249
QY 961 tggggccataggtttaatgagtcttgggaagttaagaagaagatattacaagaatgaaactgc 1020
   |||||
DB 1250 tggggccataggtttaatgagtcttgggaagttaagaagaagatattacaagaatgaaactgc 1309
QY 1021 ttacagtttgaagaagatgttgggaagatgtgcccccttggcagttccagcaattggagc 1080
   |||||
DB 1310 ttacagtttgaagaagatgttgggaagatgtgcccccttggcagttccagcaattggagc 1369
QY 1081 tggaaagaccacagctccacatagaaaaaagccacacagttcgagaatcctcactgc 1140
   |||||
DB 1370 tggaaagaccacagctccacatagaaaaaagccacacagttcgagaatcctcactgc 1429
QY 1141 gacacaaagcgagacgaagatcattagtgcaagttgccaatgtgcagcagctggtgaaaa 1200
   |||||
DB 1430 gacacaaagcgagacgaagatcattagtgcaagttgccaatgtgcagcagctggtgaaaa 1488
QY 1201 ccctgagggagaccacacttgcgcacatgatataggaagaccctatcagaagac 1260
   |||||
DB 1489 ccctgagggagaccacacttgcgcacatgatataggaagaccctatcagaagac 1488
QY 1261 tctccctgacttaaacangaatctcctgtgwaatcccaaatgttagtcctaaatctgca 1320
   |||||
DB 1549 tct-cctgactttaaagc--aatcctgtlagaatcccaatgt--agtcctaaatctgca 1603
QY 1321 attatgagggctaacacatgaaatcttcttccagccaatcaagtcgttgaacgctg 1380
   |||||
DB 1604 attatgagggctaacacatgaaatcttcttccagccaatcaagtcgttgaacgctg 1663
QY 1381 gcttttttgaagaagtgtatgagcattgtttatagatgctggtagaagtagaagatgta 1440
   |||||
DB 1664 gcttttttgaagaagtgtatgagcattgtttatagatgctggtagaagtagaagatgta 1723
QY 1441 aacttgtaaaagataatctaaatctcatagttctcagttataaattttctctgtc 1500
   |||||
DB 1724 aacttgtaaaagataatctaaatctcatagttctcagttataaattttctctgtc 1783
QY 1501 ccggaatt 1508
   |||||
DB 1784 ccgcaatt 1791

```

RESULT 4
AAI36580
ID AAI36580 standard; DNA; 1921 BP.
XX

```

AC AAI36580;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #5266 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN MO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236559.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR.
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID NO 5266; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
XX CC The present sequence is one such probe. The probes are useful for
XX CC producing a microarray for predicting, measuring and displaying gene
XX CC expression in samples derived from human placenta. The probes are useful
XX CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;

```

Query Match 95.2%; Score 1436.6; DB 22; Length 1921;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1488; Conservative 2; Mismatches 12; Indels 6; Gaps 4;

```

QY 1 ttactactaaaactactgtagatcccttaaggcacagcaagaatgagctattacgac 60
   |||||
DB 290 ttactactaaaactactgtagatcccttaaggcacagcaagaatgagctattacgac 349
QY 61 agcagctatcataattatcaatgtcgagcgaacaaataccagctaccccgacagacat 120
   |||||
DB 350 agcagctatcataattatcaatgtcgagcgaacaaataccagctaccccgacagacat 409
QY 121 atagctgagaagaagaagcaagaagcagattacttacaagaatgtagcagtgtatgtc 180
   |||||
DB 410 atagctgagaagaagaagcaagaagcagattacttacaagaatgtagcagtgtatgtc 469
QY 181 tacttcaagacatttttggagaatggggaagctatgttggatccttcacacactct 240
   |||||
DB 470 tacttcaagacatttttggagaatggggaagctatgttggatccttcacacacactct 529
QY 241 gtgacaccaagtggcgcatatgttgtatgatatcttcttatcttatctctctgtg 300
   |||||
DB 530 gtgacaccaagtggcgcatatgttgtatgatatcttcttatcttatctctctgtg 589
QY 301 ttgatatgtgctctgtcttcttggctcatagcctttcatcatatgtagcgatcattaaatgat 360
   |||||
DB 590 ttgatatgtgctctgtcttcttggctcatagcctttcatcatatgtagcgatcattaaatgat 649

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QY 361 ccagacatcacacttggtgtgacacagctccattcttcacagggcctttgtctcc 420
 Db 650 ccagacatcacacttggtgtgacacagctccattcttcacagggcctttgtctcc 709
 QY 421 ctgaagaccccaaacacacatgagatggtatgctgtgttactgaagatgtctctg 480
 Db 710 ctgaagaccccaaacacacatgagatggtatgctgtgttactgaagatgtctctg 769
 QY 481 gcccgtcctcagtgatgctcctcagtcacatcttcaagltgacatataatcttcaat 540
 Db 770 gcccgtcctcagtgatgctcctcagtcacatcttcaagltgacatataatcttcaat 829
 QY 541 ggaagctgcttgcccaaaatggaactgtctgaaagagagcccaacatcgtttcagc 600
 Db 830 ggaagctgcttgcccaaaatggaactgtctgaaagagagcccaacatcgtttcagc 889
 QY 601 tactttgacttatagatgagatggaagcttgcctcatgttgccgcatgtgtat 660
 Db 890 tactttgacttatagatgagatggaagcttgcctcatgttgccgcatgtgtat 949
 QY 661 ttccgccaacacacagctgtgtagaagaaagctttagagcccaactctccgtatatacaga 720
 Db 950 ttccgccaacacacagctgtgtagaagaaagctttagagcccaactctccgtatatacaga 1009
 QY 721 gacagtgaaagggagatgacatgagctttaaagaccccaaatgtgtaacagccaatc 780
 Db 1010 gacagtgaaagggagatgacatgagctttaaagaccccaaatgtgtaacagccaatc 1069
 QY 781 atccggtcaccgccgtagaactgttccatgaaatgagcaagagccctctgtatgcc 840
 Db 1070 atccggtcaccgccgtagaactgttccatgaaatgagcaagagccctctgtatgcc 1129
 QY 841 cttagaccgaagcagtagaagcaaaagataactttagaatttggtagacttatactact 900
 Db 1130 cttagaccgaagcagtagaagcaaaagataactttagaatttggtagacttatactact 1189
 QY 901 ggtgattccacttggaacatctccaatctagaagctcctatgttcccgaraattctc 960
 Db 1190 ggtgattccacttggaacatctccaatctagaagctcctatgttcccgaraattctc 1249
 QY 961 tgggagcctaggtttaagatgtcttggaaagttagaggaagtattacaagtgaactgc 1020
 Db 1250 tgggagcctaggtttaagatgtcttggaaagttagaggaagtattacaagtgaactgc 1309
 QY 1021 ttacagtttgaaggaagtgtagaagatataagcccttcttgagtgccaagaatttgagc 1080
 Db 1310 ttacagtttgaaggaagtgtagaagatataagcccttcttgagtgccaagaatttgagc 1369
 QY 1081 tggaaagaccagcagctcacatagaaaaagacacacagcttcgagaatccctgcagctcg 1140
 Db 1370 tggaaagaccagcagctcacatagaaaaagacacacagcttcgagaatccctgcagctcg 1429
 QY 1141 gacacaaagcgagagcgaagtcatttagtgcaattgcatgttcagcagcgtgtgtaaa 1200
 Db 1430 gacacaaagcgagagcgaagtcatttagtgcaattgcatgttcagcagcgtgtgtaaa 1488
 QY 1201 cccctgagagaccacacacttccgcaacacatgaaataggaacaacacttataagaagc 1260
 Db 1489 cccctgagagaccacacacttccgcaacacatgaaataggaacaacacttataagaagc 1548
 QY 1261 tctccctgacttaaaanagaatctctgttwaatcccaaatggttgccttaaatgtga 1320
 Db 1549 tct-cctgactttaaagc--aattctgttagaattcccaaatgt--agtccttaattgca 1603
 QY 1321 attatgagggcaccacacttaatttattctttagccaatcaaatgctgttgaacagctg 1380
 Db 1604 attatgagggcaccacacttaatttattctttagccaatcaaatgctgttgaacagctg 1663
 QY 1381 gcttttttgaaggtgtatgctatgttttatgatgatgctggtgtaagagtaagta 1440
 Db 1664 gcttttttgaaggtgtatgctatgttttatgatgatgctggtgtaagagtaagta 1723
 QY 1441 aactgtgtaaaagataacttaaaatctcatagttctcagttataaaattttcttgtt 1500

Db 1724 aactgtgtaaaagataacttaaaatctcatagttctcagttataaaattttcttgtt 1783
 QY 1501 ccggaatt 1508
 Db 1784 ccgcaatt 1791
 RESULT 5
 AAS92631
 ID AAS92631 standard; cDNA; 1395 BP.
 AC AAS92631:
 XX
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #28435.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HXSE-) HXSEQ INC.
 PI Drmanac RF, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 DR P-PSDB: ABC28444.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 1: SEQ ID No 28435; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_ptc_sequences.
 XX
 SQ Sequence 1395 BP; 410 A; 319 C; 299 G; 367 T; 0 other:
 Query Match 83.5%; Score 1259.4; DB 23; Length 1395;
 Best Local Similarity 99.2%; Pred. No. 0;

Query Match	80.58;	Score 1214.4;	DB 22;	Length 1257;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 1249; Conservative	2;	Mismatches 4;	Indels 4;	Gaps 3;

Qy	46	atgagcattacgagcagcgcatacatatatactgagcgcaaaataccaggtac	105
Db	1	atgagcattacgagcagcgcatacatatatactgagcgcaaaataccaggtac	60
Qy	106	ccgcgaagcaccttataagctggaagagaagaagacaagacgaatcattcaccaagat	165
Db	61	ccgcgaagcaccttataagctggaagagaagaagacaagacgaatcattcaccaagat	120
Qy	166	ggcagctgtatagttacttcaagcacatttttggagaatggggagctatgtgttac	225
Db	121	ggcagctgtatagttacttcaagcacatttttggagaatggggagctatgtgttac	180
Qy	226	atcttaccaccttttggacaaccaagttggcgccatagtgttgatattttcttct	285
Db	181	atcttaccaccttttggacaaccaagttggcgccatagtgttgatattttcttct	240
Qy	286	tatatctccgctgtgtgataatttggctcctgtcttcttggctataagcctttcacagc	345
Db	241	tatatctccgctgtgtgataatttggctcctgtcttcttggctataagcctttcacagc	300
Qy	346	gattctataatgataccagacatcacacctgtgttgacaagtcattcttccaag	405
Db	301	gattctataatgataccagacatcacacctgtgttgacaagtcattcttccaag	360
Qy	406	gaccttttgttcccttaagagaccacaacacatagagataagttacgtgtacgttact	465
Db	361	gaccttttgttcccttaagagaccacaacacatagagataagttacgtgtacgttact	420
Qy	466	gaagaatgtctgttggcgctgtctcatgtgtgatactccctccatcttaagtgtcatata	525
Db	421	gaagaatgtctgttggcgctgtctcatgtgtgatactccctccatcttaagtgtcatata	480
Qy	526	ataccttatacttggagctgtccttgggccaaaatgagcaactgtctcgaaagagcccaa	585
Db	481	ataccttatacttggagctgtccttgggccaaaatgagcaactgtctcgaaagagcccaa	540
Qy	586	accattgtttcagctcatttgcactataagataagagatgaggaagcctttgcctatg	645
Db	541	accattgtttcagctcatttgcactataagataagagatgaggaagcctttgcctatg	600
Qy	646	tggcgcaatgtgcatlcttcggccaacacagctgtgtagaagagacaagttagagcccaact	705
Db	601	tggcgcaatgtgcatlcttcggccaacacagctgtgtagaagagacaagttagagcccaact	660
Qy	706	ctcgcgtatacacaagaacaaatgaagagagatgacgatgacatttaagaccttaaatia	765
Db	661	ctcgcgtatacacaagaacaaatgaagagagatgacgatgacatttaagaccttaaatia	720
Qy	766	gtccaaagcacaaatcatccctgtgtcaccgccggttaactatgttccatgaaatgacaaatgag	825
Db	721	gtccaaagcacaaatcatccctgtgtcaccgccggttaactatgttccatgaaatgacaaatgag	780
Qy	826	agccctctgtatgaccttgacgcgcaagaagctagcccaagaataactttgagatttgg	885
Db	781	agccctctgtatgaccttgacgcgcaagaagctagcccaagaataactttgagatttgg	840
Qy	886	acatttatactgtgtgataccacttggacaatcaccacaatcagaagctccatggt	945
Db	841	acatttatactgtgtgataccacttggacaatcaccacaatcagaagctccatggt	900
Qy	946	ccccggaataatctcttggggccataggtttaatgatagttcttggaaagttaaggaaat	1005
Db	901	ccccggaataatctcttggggccataggtttaatgatagttcttggaaagttaaggaaat	960
Qy	1006	tacaaagtgaactgcttacaagtttgaagaagatgtggaagataatgccccctttgca	1065
Db	961	tacaaagtgaactgcttacaagtttgaagaagatgtggaagataatgccccctttgca	1020

QY	1066	gcctaaagcaattgagcttgcgtgaaagcgcgcgcgcgtctccatatatgaaaaagcccccacagatttga	1125
Db	1021	gcccagcaagcatcttgagctctgtgaaagcaccgcagctctccacataatgaaagcaccaccagttccga	1080
QY	1126	gaatctccgcagctctgcgcgcacacaaagcgcgagagacgaaggtctcatcttagtctgcagcttgcacatttc	1185
Db	1081	gaatctccgcagctctgcgcgcacacaaagcgcgagagacgaaggtctcatcttagtctgcagcttgcacatttc	1140
QY	1186	agcagcctgtgtgaaaaacccctcgtagagagagacacacatttcgcgcacatatgatatagggaaac	1245
Db	1141	agcagcct-gtctaaaaacccctcgtagagagacacacacatttcgcgcacatatgatatagggaaac	1199
QY	1246	accttatatagaagaagctctccctctgactttaaacaangaatcctctgtctggaatccccaattgt	1304
Db	1200	accttatatagaagaagctctcctgactttaaacaag--aatctctgtctggaatccccaattgt	1255

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XX RESULT 7
XX ID AAK17807
XX AAK17807 standard; DNA; 1118 BP.
XX
XX AAK17807;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe SEQ ID NO: 17798.
XX
XX Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0633666.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
XX Example 4; SEQ ID NO: 17798; 650pp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
XX Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;
XX
XX
XX Query Match 70.9%; Score 1069.6; DB 22; Length 1118;
XX Best Local Similarity 99.9%; Pred. No. 9.7e-302;
XX Matches 1069; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 301 ttgatattgctctctcttttgctcatagccttccatcagtcgcatctataatgat 360
Db 349 ttgatattgctctctcttttgctcatagccttccatcagtcgcatctataatgat 408
QY 361 ccagacatcaacacttgcttgacaagtcacatctcttccacagggcctttgtctcc 420
Db 409 ccagacatcaacacttgcttgacaagtcacatctcttccacagggcctttgtctcc 468
QY 421 cttagagaccacaacacatagatgatatgctgtgttaccggaagaatgtctg 480
Db 469 cttagagaccacaacacatagatgatatgctgtgttaccggaagaatgtctg 528
QY 481 gccgtgcatatgctgctccagtcacatcttaagtgtcatalcataatccttaccat 540
Db 529 gccgtgcatatgctgctccagtcacatcttaagtgtcatalcataatccttaccat 588
QY 541 ggaagctgcttgagccaataatgcaactgctcgaagaagagcccaacatctgttccagc 600
Db 589 ggaagctgcttgagccaataatgcaactgctcgaagaagagcccaacatctgttccagc 648
QY 601 tacttgacatcatagatgatatgagaatggaaagcttgccatgtgagcattgtgat 660
Db 649 tacttgacatcatagatgatatgagaatggaaagcttgccatgtgagcattgtgat 708
QY 661 ttccgccaacacacagctgtgtagaagaagacagtagagcccaactctccgcatatacaga 720
Db 709 ttccgccaacacacagctgtgtagaagaagacagtagagcccaactctccgcatatacaga 768
QY 721 gacagatgaagagagatagacatgacatgatttaagacccaatgattgttaacagccaatc 780
Db 769 gacagatgaagagagatagacatgacatgatttaagacccaatgattgttaacagccaatc 828
QY 781 atccgagtcacacccgctgaactatgtccatgaatgaacagtagagccctctgtatgac 840
Db 829 atccgagtcacacccgctgaactatgtccatgaatgaacagtagagccctctgtatgac 888
QY 841 cttagacgcaaaagcagtagccaagaataacttggagatttggtagacattatctataact 900
Db 889 cttagacgcaaaagcagtagccaagaataacttggagatttggtagacattatctataact 948
QY 901 ggtggttccactgagacatctcaccacatctagaagctcctcctggtcccgaraaatcttc 960
Db 949 ggtggttccactgagacatctcaccacatctagaagctcctcctggtcccgaraaatcttc 1008
QY 961 tggggccataggtttaatgatgtcttggaaagttaagaggaaatattacaagaatgacatgc 1020
Db 1009 tggggccataggtttaatgatgtcttggaaagttaagaggaaatattacaagaatgacatgc 1068
QY 1021 ttacagtttgaagaagatgctggaagatataatgcccccttgcagtgccaa 1070
Db 1069 ttacagtttgaagaagatgctggaagatataatgcccccttgcagtgccaa 1118

```

RESULT 9

AAF85050
ID AAF85050 standard; cDNA: 1257 BP.

AAF85050;
AC

09-JUL-2001 (first entry)

Nucleotide sequence of a rat Kir5.1 polypeptide.

Kir5.1: inwardly rectifying potassium channel; ion channel;

renal failure; hypokalemia; hypertension; hypotension; thyroid disease;

pancreatitis; ss.

Rattus sp.

Key
CDS

Location/Qualifiers
1..1257
/*tag= a

```

FT /product= "Kir5.1"
FF /note= "no termination codon given"
PN
XX MO200125258-A1.
PD 12-APR-2001.
XX
XX 29-SEP-2000; 2000MO-US26996.
XX
XX 04-OCT-1999; 99US-0157491.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Swanson RJ, Liu Y, McKenna E;
PI MPI: 2001-290604/30.
DR P-PSDB: AAB68277.
XX
XX Novel nucleic acid encoding human Kir5.1 subunit protein useful for
PT Identifying activators and inhibitors of potassium channels containing
PT the protein subunit useful for treating various diseases
XX
XX Disclosure: Fig 4A-B: 52pp; English.
XX
XX The present sequence encodes a rat Kir5.1 subunit protein. Kir5.1
XX is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
XX are useful for identifying inhibitors or activators of potassium
XX channels. Kir5.1 proteins are useful as attractive targets for drug
XX discovery and as valuable research tools for understanding ion channel
XX biology. Kir5.1 proteins are also useful for identifying inhibitors or
XX activators of potassium channels. Inhibitors or activators screened
XX using Kir5.1 protein are useful for treating a variety of diseases
XX CC involving excessive or insufficient potassium channel activity, such as
XX renal failure, hypokalemia, hypertension, hypotension, thyroid disease
XX and pancreatitis.
XX
XX Sequence 1257 BP; 325 A; 325 C; 314 G; 293 T; 0 other:
SQ

```

Query Match 57.6%; Score 869.6; DB 22; Length 1257;
Best Local Similarity 82.6%; Pred. No. 2.5e-243;
Matches 1030; Conservative 1; Mismatches 211; Indels 5; Gaps 3;

```

QY 46 atgagctattacgagcagcatatattcaatgcgacgcaaaataccagagctac 105
Db 1 atgagctattacgagcagcatatattcaatgcgacgcaaaataccagagctac 60
QY 106 ccgcagagcacatratatagctgagaagaagaagaagcgcgttacttccacaaagt 165
Db 61 ccgcagagcacatratatagctgagaagaagaagaagcgcgttacttccacaaagt 120
QY 166 ggcagctgtaattgtctacttcaagcacatlttggagaatggggaagtatgtgtgac 225
Db 121 ggcagctgtaattgtctacttcaagcacatlttggagaatggggaagtatgtgtgac 180
QY 226 atcttcacacactctgttgacaacagtguggcacatagtgtgtatatttcttacc 285
Db 181 atcttcacacactctgttgacaacagtguggcacatagtgtgtatatttcttacc 240
QY 286 tatattctctgtgtgatatatttgctctgtcttggctatagccttataatgac 345
Db 241 tatattctctgtgtgatatatttgctctgtcttggctatagccttataatgac 300
QY 346 gatctaatgaatcagacacacacacttgcttgtaacacgctccatcttccacag 405
Db 301 gatctaatgaatcagacacacacacttgcttgtaacacgctccatcttccacag 360
QY 406 gccctttgttctccctagagacccaacacacatagatatgtatcgtgtgtact 465
Db 361 gccctttgttctccctagagacccaacacacatagatatgtatcgtgtgtact 420
QY 466 gaagaatgtctgtgacgtgtgctatgtgataccctccagtcacatgaatgtgacata 525

```

Db	421	gaagaatgctcgtctggccggtgcgaagctcatcccttcagttccatcccttgagctgcatcata	486
Oy	526	aataccttcatcttgagagctgcctctggcccaaatgycaaactgctcgaaagagaccocaa	585
Db	481	aacaccttcatcttgaggagccttggcacaagaatgycgaccgccggaagcagaccag	540
Oy	586	accattcgttccgctaacttgcacttaagtaagagagatgaggagccttgcctcatg	645
Db	541	accatccgcttcgctatttctgcgacatccctggcatgagagagcgggaaccttgcctcatg	600
Oy	646	tggagcaatgggtaatttctggcccaaaccccggtgtagaaggagacaggttaaggcccaactt	705
Db	601	tggcgcaataggtaacttccgcgacccgaaccacccgtgtggtagggagcaggtgtaggcccactt	660
Oy	706	ctccgcctatccagaagacagctgaaggagagatgacagatgcatctttaaagactcaatata	765
Db	661	ctggcgctatccagaagacagcgaagaaggcggatggaagatggtggtttaaagacctcaaatc	720
Oy	766	gtcaacagccaatcatcatctgtgcaaccccggttaactatgtlccatgtaaatgtgacatag	825
Db	721	gtcaatgaccgaataatccgtgtaacgcaagcgagacatgttccatgaatatgtgacacagag	780
Oy	826	agccctctgtatgccccttgacgcgcaaaagcagtagcccaagaataacttggagatttgggtg	885
Db	781	agtcctctgtatgccccttgacgcgcaaaagcagtagcccaagaataatttcgagattcctggtg	840
Oy	886	acattatctcatctggtgtaattccactggaacaatctcaccaatctagaagctcctcatggt	945
Db	841	acattatctcatctggtgtaacttactactggaacatccacacagttccagaagttcctacgtc	900
Oy	946	ccccgataaattctctgggggacataggtttaatgatgtcttggaaagttaagagaaatgat	1005
Db	901	ccccgataaattctcttgggggacacagaagttctcatgtatcttggaaagtbaagagaaatgac	960
Oy	1006	tacaagaatgaaactgcgtacaggttggaggaagatgtggaagatatagccccctttgcaggt	1065
Db	961	tacaagaatgaaactgcgtctgcaggttgggggaagcgtggaagtttaacgccccctttgcaggt	1020
Oy	1066	gcccaagaatttgacttggaaagacacgacgcagcttcaca---tagaaaaagcaccacaggt	1122
Db	1021	gcccaacaacttgcacttggaaagacacacagctcacaacacttggagaaaaagcttccctgcgc	1080
Oy	1123	cggagaatctgcagcgttcgagacaccaaagcggagacgaagtgcaattagtgtgcagttgcactt	1182
Db	1081	cggagaatctgcagccttcgagacaccaaacacacagagagagcttccttaagcaggttgcacgt	1140
Oy	1183	gtcgcgcgcgtggtgaaaaaccttgaagagacccacacttctgcgcaacacttgatataagga	1242
Db	1141	gtgcgcgcgcgt-gtgcgaagaccagagagacagcgtctgtcccaagaatgtggttgaagga	1199
Oy	1243	aacaccttcatcaaaagccttcccttgaactttaaangaatcctctgt	1289
Db	1200	gtctccctatcagaagaagccct-ctgtgaactttaaagcagatctcctcatg	1245

```

RESULT 10
AAK35739
ID AAK35739 standard; cDNA; 907 BP.
XX
AC AAK35739;
XX
DT 09-JUL-1999 (first entry)
XX
DE cDNA encoding a protein identified by the signal sequence trap method.
XX
KW Signal sequence trap method; SSR method; immunisation; inhibition;
KW infection; allergy; cancer; regulation; tissue formation; tissue repair;
KW activin activity; inhibin activity; chemokine activity;
KW cytokine activity; blood coagulation regulation; agonist; antagonist;
KW metabolic disorder; hormonal disorder; immune disorder;
KW severe combined immunodeficiency; SCID; AIDS; Thrombosis; cancer;
KW wound; ss.
XX

```

OS Homo sapiens.
XX
PN W09910126-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98WO-JP04514.
XX
PR 07-OCT-1997; 97JP-0274674.
XX
PA (ONOCY) ONO PHARM CO LTD.
XX
PI Fukushima D, Shibayama S, Tada H;
XX
DR WPI: 1999-277254/23.
XX
PT P-PSDB: AAY02380.
XX
PS Polypeptides identified by the signal sequence trap method from a
XX human cDNA library
XX
XX Claim 4; Page 213-215; 201pp; Japanese.

CC AAX35656-X35747 represent cDNA sequences that encode novel polypeptides
CC (AAV02358-84) which are identified from a human placental cDNA library
CC by the signal sequence trap (SST) method. The polypeptides have a
CC broad range of physiological activity, including immunisation against
CC and inhibition of infections, allergies and cancer; regulation of tissue
CC formation and repair; activin/inhibin activity; chemokine/cytokine
CC activity; blood coagulation regulation; and receptor/ligand agonist
CC or antagonist activity. The polypeptides can be used for prevention
CC and treatment of disorders including infections by bacteria, yeasts and
CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;
CC immune disorders (including severe combined immunodeficiency (SCID)
CC and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
XX
XQ Sequence 907 BP; 278 A; 210 C; 183 G; 236 T; 0 other;

[illegible]

DE XX Human diagnostic and therapeutic polynucleotide (DITHP) #102.

XX KW Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;

KW cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;

KW acquired immune deficiency syndrome; AIDS; autoimmune disorder;

XX respiratory disorder; ss.

OS Homo sapiens.

PN WO200162927-A2.

PD 30-AUG-2001.

XX 21-FEB-2001; 2001WO-US06059.

PF 24-FEB-2000; 2000US-0184693.

XX 24-FEB-2000; 2000US-0184697.

XX 24-FEB-2000; 2000US-0184698.

PR 24-FEB-2000; 2000US-0184768.

PR 24-FEB-2000; 2000US-0184769.

PR 24-FEB-2000; 2000US-0184770.

PR 24-FEB-2000; 2000US-0184771.

PR 24-FEB-2000; 2000US-0184772.

PR 24-FEB-2000; 2000US-0184773.

PR 24-FEB-2000; 2000US-0184774.

PR 24-FEB-2000; 2000US-0184776.

PR 24-FEB-2000; 2000US-0184777.

PR 24-FEB-2000; 2000US-0184797.

PR 24-FEB-2000; 2000US-0184813.

PR 24-FEB-2000; 2000US-0184837.

PR 24-FEB-2000; 2000US-0184841.

PR 24-FEB-2000; 2000US-0185213.

PR 24-FEB-2000; 2000US-0185216.

PR 12-MAY-2000; 2000US-0203785.

PR 15-MAY-2000; 2000US-0204226.

PR 16-MAY-2000; 2000US-0204525.

PR 16-MAY-2000; 2000US-0204821.

PR 16-MAY-2000; 2000US-0204908.

PR 16-MAY-2000; 2000US-0205232.

PR 17-MAY-2000; 2000US-0204815.

PR 17-MAY-2000; 2000US-0204863.

PR 17-MAY-2000; 2000US-0205221.

PR 17-MAY-2000; 2000US-0205285.

PR 17-MAY-2000; 2000US-0205286.

PR 17-MAY-2000; 2000US-0205287.

PR 17-MAY-2000; 2000US-0205323.

PR 17-MAY-2000; 2000US-0205324.

XX (INCYTE) INCYTE GENOMICS INC.

PA Panzer SR, Spiro PA, Banyille SC, Shah P, Chalup MS, Chang SC;

XX Chen A, D'Sa SA, Amshery S, Dahl CR, Dam TC, Daniels SE;

PI Dufour GE, Flores V, Fong WT, Greenwalt LB, Hallman JL, Jones AL;

PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daiffo A;

PI Wright RJ, Yap PE, Yu YJ, Bradley DL, Bratcher SR, Chen W;

PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;

XX WPI: 2001-502867/55.

DR P-PSDB; AAU19516.

XX Polynucleotides encoding diagnostic and therapeutic proteins, e.g.

XX enzymes, hormones and receptors, useful in diagnostics and therapeutics

PT -

XX

PS Claim 1: Page 340-341; 522pp; English.

XX

XX The invention relates to polynucleotides (I) encoding diagnostic and

CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes,

CC and proteins involved in growth and development and receptors (I') and

CC (II) may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate DITHP expression. For example, (I) and

CC (II) may be used to treat disorders associated with decreased polypeptide

	Query Match	28.5%	Score 430;	DB 22;	Length 856;
	Best Local Similarity	100.0%;	Pred. No. 4,4e-115;		
	Matches 430;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 ttactactacaaanaactacctgcatcccttaaggagacagcaagaatgagctatttaggc	60			
DB	427 ttactactacaaanaactacctgcatcccttaaggagacagcaagaatgagctatttaggc	486			
QY	61 agcagctatcatatatacatatcgtgagcgcaaaatacccaagctaccgcgcagagcacatt	120			
DB	487 agcagctatcatatatacatatcgtgagcgcaaaatacccaagctaccgcgcagagcacatt	546			
QY	121 atagctgagaaagagagagcaagaacgattacttcacaaagatgacgctgtaatgctc	180			
DB	547 atagctgagaaagagagagcaagaacgattacttcacaaagatgacgctgtaatgctc	606			
QY	181 tacttcaagcacatttttggagaatgagggaagctatgtgtgtgacatcttcaaccactctt	240			
DB	607 tacttcaagcacatttttggagaatgagggaagctatgtgtgtgacatcttcaaccactctt	666			
QY	241 gtggagaccagaatgaggcgcatalgttttgatatttcttactatattccctcgtag	300			
DB	667 gtggagaccagaatgaggcgcatalgttttgatatttcttactatattccctcgtag	726			
QY	301 ttgatatttgctctgctcttttggctcatalagcctttcatalcatalgacatctataaagat	360			
DB	727 ttgatatttgctctgctcttttggctcatalagcctttcatalcatalgacatctataaagat	786			
QY	361 ccagagcatcacacctgtgtgtgacaagatcattctttccacaggggacctttgtctccc	420			
DB	787 ccagagcatcacacctgtgtgtgacaagatcattctttccacaggggacctttgtctccc	846			
QY	421 ctgagagacc 430				
DB	847 ctgagagacc 856				
RESULT	13				
ID	AAH21453				
XX	AAH21453 standard; DNA; 1284 BP.				
AC	AAH21453;				
XX	18-SEP-2001 (first entry)				
DT	Human IRK1 DNA.				
DE					
XX	Inhibitor: eukaryotic; potassium channel; TRK1; TRK2; TOK1;				
FW	activator: ds.				
XX					

OS Homo sapiens.
 PN MO200151519-A2.
 XX 19-JUL-2001.
 PD 05-JAN-2001; 2001WO-EP00055.
 XX 11-JAN-2000; 2000DE-1000651.
 PR (AVET) AVENTIS PHARMA DEUT GMBH.
 XX Leberer E, Leeuw T, Ritscher A;
 XX WPI: 2001-442137/47.
 DR Identifying inhibitors and activators of eukaryotic potassium channels,
 PT for use as pharmaceuticals, comprises using yeast cells that express
 PT heterologous, but no endogenous, potassium channels -
 XX Disclosure: Page 46; 78pp; German.
 PS
 XX This sequence represents a novel method for identifying inhibitors or
 CC activators (A) of a eukaryotic potassium channel (KC) by applying a test
 CC compound to a mutant *Saccharomyces cerevisiae* cell in which: (1) the
 CC three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (11) a
 CC eukaryotic KC is expressed heterologously, where the effect of the
 CC compound on the eukaryotic KC is then determined. The method is used to
 CC identify inhibitors or activators (A) of a eukaryotic potassium channel;
 CC (A) are potentially useful as pharmaceuticals. The method is easily
 CC automated for parallel processing of many samples, using either different
 CC concentrations of test compounds and/or different levels of heterologous
 CC gene expression. It allows identification of compounds that inhibit human
 CC KC selectively. This sequence represents the human IRK1 encoding DNA
 CC described in the method of the invention.
 XX
 SQ Sequence 1284 BP; 345 A; 269 C; 322 G; 348 T; 0 other;

Query Match 20.8%; Score 314.2; DB 22; Length 1284;
 Best Local Similarity 60.4%; Pred. No. 3.4e-81;
 Matches 577; Conservative 1; Mismatches 359; Indels 18; Gaps 3;

QY 142 agaagagcattacttcacaaagatgacgctgtaagtctactcaagcattttgga 201
 DB 130 aggaagccctgttgaagaagaatgacactgtaattcgaattcaagctgggga 189
 QY 202 gaatgggaagctatggtgtacattcaccactctgttgacaccaaagtgagccat 261
 DB 190 aaggagacaagctacattgacatttactacgtgtgtgacattcgctggcggtg 249
 QY 262 atgttgcataattcttctataattcctcgtgtgattatgtgctctctt 321
 DB 250 atgcgtgatacttctgctagcttcttctcctcgtggtgttcttggcggtgtt 309
 QY 322 tggctatagccttcacatgagcattatgaatgacacacacacacacacacac 381
 DB 310 tggctatagccttcacatgagcattatgaatgacacacacacacacacacac 369
 QY 382 gacacagcattcttcaagagggccttctgttccctcctagacacacacacata 441
 DB 370 tctggaggtcaaacagctcagcagccttcttctcattgagacacacacacacac 429
 QY 442 ggaatagctatgcgtgttactgaagaatgtctgtgacgctgctacatgtgaccc 501
 DB 430 ggcatagggtccgattggtcagcagatgaatgccgattggtgttcatgtgtcttc 489
 QY 502 cagtcacattcaagltgacatacaacattatcattgagcgtgcttggcccaaatg 561
 DB 490 cagtcacattggtgctgacataatgattatcattgagcgtgcttggcccaaatg 549
 QY 562 gcaatgtcgaagaagacacacacattgcttcaagctacattgacattatgattag 621

DB 550 gcaaaagccaaagaaagaaatgagactcttcttcacgtacaaatgctgtgaccatg 609
 QY 622 agaatgtgaaagccttgcctcatgtggtcattgtgatttccggccaacacgttga 681
 DB 610 agaatgtgaaagccttgcctcatgtggtcattgtgatttccggccaacacgttga 669
 QY 682 gaagaaacagltagagcccaactctcgcgtatagacaaagacagtgaagg---agagtg 738
 DB 670 gaagtcacattgagcccgagctcctcaatccagaattacttctgaagggataacalc 729
 QY 739 acgatggtcattaaagactcaaatagtc-----aagaccaatcctccg 786
 DB 730 ccccttgatcaataatgacaaatgltgtgttgacagltggaattgacagctatcttg 789
 QY 787 gtcaccccgtaactattgcacaaatgacacagccctgtatgacctgtgac 846
 DB 790 gtaaccacatcattggtcattgataatagtgatgagatgacattatgattgagc 849
 QY 847 cgcaaaagcagtgccaaagataacttggagatttgggtacattatctatctactgtgat 906
 DB 850 aagcagacattgataatgcagacttggaaattgtgtgatactagaagcgatgtgga 909
 QY 907 tccactggaacatctcacaactagaagctctatgttcccgaraattctctgggac 966
 DB 910 ggcactgcatagacaacacagltgtgtgtatttatttggccaagagatccttctgggac 969
 QY 967 ctaagttaatgagtgtcttgaaatgaagaaagatatacaaaagtgaactgtctacag 1026
 DB 970 ccccgatagacacagtgctctttagagaaagacactactataaaagtgaactgtctacag 1029
 QY 1027 ttgaaaggaagtgtggaagta---tatgcccttcttgagtgccaagaactgg 1078
 DB 1030 ttctataagacttaagaaagtaaccacactccctttagtgagcagagacttag 1084

RESULT 14

ABA35969 ID ABA35969 standard; DNA; 1310 BP.
 XX ABA35969;
 AC
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Probe #14435 for gene expression analysis in human heart cell sample.
 XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200157274-A2.
 XX 09-AUG-2001.
 PD
 XX
 PF 30-JAN-2001; 2001WO-US00066.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI: 2001-488899/53.
 DR Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts -
 PT

XX Claim 4: SEQ ID NO 14435; 530bp; English.

XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging, the
 CC monitoring and prognosis diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

Query Match 20.2%; Score 304.4; DB 22; Length 1310;
 Best Local Similarity 59.0%; Pred. No. 2.5e-78;
 Matches 584; Conservative 1; Mismatches 387; Indels 18; Gaps 3;

QY 142 agaagacgacttcaacaagaatgagcgtgaatgctactcaagcaaatlttga 201
 DB 156 agagccgcttctgaagaagaatgagcactgaatgttcatcattcaatgtgtgag 215
 QY 202 gaatgggaagcgtatggtgacatcttaccactcttctggaaccacagtggccat 261
 DB 216 aaggggaaacggaaccccgagacatcttaccacgtgtgtgacatcgtgcggtg 275
 QY 262 atcttgatgattcttcttcttcttcttctctctctggtgattgtgctgcgtctt 321
 DB 276 atgctgtatctcttgcgcgcttctctctctctctctctctctctctctctct 335
 QY 322 tggcctacgttcaatcgtcgtcgtatcaatgaatccacacacacacctgtgtt 381
 DB 336 tggctgtagctctgctccatggtgacctgtagatccaaagaggaagcctgtgtg 395
 QY 382 gacaacgtcattcttcaagaggccttcttcttcttcttcttcttcttcttctt 441
 DB 396 tcgagagtcacacgcttcaacggtccttcttcttcttcttcttcttcttcttctt 455
 QY 442 ggaatggtatcgtctgttcttcttcttcttcttcttcttcttcttcttcttct 501
 DB 456 ggtatggttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 515
 QY 502 cagtcacatcttaagttgacatcaaatcattatcattggaagcgtccttggcacaatg 561
 DB 516 cagtcacatcttggcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 575
 QY 562 gcaactgctcgaagaagagcgaacacattcgttgcacacttcttgaattatagatg 621
 DB 576 gcaagcgaagaagaagaacgagactctgtcttcaatgacatgctggtgcatg 635
 QY 622 agagatgggaagcttgcacctatggtgcgcatgtgtatcttgcgcaaacacgtgta 681
 DB 636 agagagcgaagcgt 695
 QY 682 gaaggaagcgtgagccaactctcgtctacacagaagacagtggaaggaag--atg 738
 DB 696 gaagcgtatgttgcagacacgctcctcaaatcagaattccttctggaagggtatctc 755
 QY 739 agatggtcattaaagaccctcaat-----agtaacagcaacatcatctctg 766
 DB 756 ccccttgatcaaatagacacaaatgttgggttgcacagtgaatcgatctgattcttg 815
 QY 787 gtaccccggttaactatgtcctatgaatgacatagagcgtcctgtgtccctgac 846
 DB 816 gtgtcccaatcactatagcctgaatagatgaagacgctccttattatgtgtgtgt 875
 QY 847 cgcaaacgtagcccaagaataacttggagatttggtagcattatcatctatgtgtgt 906

DB 876 aaacagacattgacaacgagacttgaatcgtgtgcatcactggaagcattgtgaa 935
 QY 907 tcaactggaacattccacacatcagaagcttcttcttcccgaraatttcttgggc 966
 DB 936 gccactgccaatgagacacagctgcttcttcttcttcttcttcttcttcttctt 995
 QY 967 catggttcaatgattcttcttgaaggaaggaaggaaggaaggaaggaaggaaggaag 1026
 DB 996 caccgcatgagcctgtgcttcttgaaggaaggaaggaaggaaggaaggaaggaaggaag 1055
 QY 1027 ttgaaggaagtggaagt--atagcccttcttgcagtgccaagcaattgacttg 1083
 DB 1056 ttccacaacttgcaggaagccacacactcccttcttcttcttcttcttcttcttct 1115
 QY 1084 aagaccagcagctccacatagaanaagca 1113
 DB 1116 aagaatatatcttctcaaatgcaattca 1145

RESULT 15

AAK17341
 ID AAK17341 standard; DNA; 1310 BP.
 XX AAK17341:
 AC AAK17341:
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 17332.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001MO-US00667.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR.
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 PS Example 4: SEQ ID NO: 17332; 650bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 XX
 SO Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

Query Match 20.2%; Score 304.4; DB 22; Length 1310;
 Best Local Similarity 59.0%; Pred. No. 2.5e-78;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 01:30:25 ; Search time 1703.75 seconds
(without alignments)
11954.163 Million cell updates/sec

Title: US-09-623-304A-2
Perfect score: 1509
Sequence: 1 ttactactacaacacacc.....ttttctgtctcggaattc 1509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estf2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	569.4	37.7	858	10	BI143740 602907395
2	506.8	33.6	781	10	BI144257 602907822
3	456.4	30.2	710	10	BF780854 602105743
4	452.2	30.0	606	9	AI636030 1292403.X
5	439.6	29.1	753	10	BI143982 602908077
6	431.4	28.5	662	10	BI101237 602886939
7	429.4	28.5	686	10	BI101492 602887284
8	401	26.6	721	9	AM475637 un96409.Y
9	374.8	24.8	783	10	BF789666 602105381
10	374.4	24.8	516	10	BF411612 UT-R-BT1-
11	368.8	24.4	658	9	BB625105 BB625105-
12	354	23.5	641	9	BB643863 BB643863
13	353.8	23.4	665	10	BF789809 602105362
14	340.6	22.6	461	12	AO222870 HS_2014-A
15	330	21.9	527	10	BF194884 708902.X
16	330	21.9	651	9	BB644922 BB644922
17	314.6	20.8	1001	10	BI546348 603188840

18	308.6	20.5	690	10	BI101289
19	297.8	19.7	641	9	BB622505 BB622505
20	295.8	19.6	533	9	AM226791 um62603.Y
21	294.4	19.5	599	9	AM318913 un09603.Y
22	292.8	19.4	525	9	AI227094 u11911.Y
23	277.4	18.4	398	9	AI747352 u105605.Y
24	277	18.4	278	12	B59110 CIT-HSP-201
25	269.8	17.9	740	9	AV602053 AV602053
26	266.8	17.7	575	9	AV603377 AV603377
27	264.6	17.5	484	9	AA989815 uc79607.Y
28	261.6	17.3	899	10	BF780894 602105404
29	249.8	16.6	2462	11	AK017299 Mus muscu
30	249	16.5	442	9	AM259025 um76601.Y
31	249	16.5	645	9	AI788269 uK56804.Y
32	247.4	16.4	493	9	AM259349 um92402.Y
33	247.4	16.4	526	9	AM012077 um07603.Y
34	226.2	15.5	411	9	AV603376 AV603376
35	226	15.0	349	9	AM475246 un63609.Y
36	226	15.0	753	12	CNS03W7V Tetraodon
37	219.4	14.5	433	9	BB848349 BB848349
38	218	14.4	702	10	BI553872 603190831
39	215.2	14.3	1190	10	BF789199 602105087
40	209.4	13.9	430	12	AQ245235 HS_2057-B
41	208.4	13.8	494	12	A2825911 2M0101B19
42	205.4	13.6	444	9	AM318491 um98406.Y
43	189.6	12.6	336	9	AI271845 q188411.X
44	185.6	12.3	687	9	AI647481 uK42610.X
45	180	11.9	780	10	BI100286 602885751

ALIGNMENTS

RESULT 1
LOCUS BI143740 858 bp mRNA linear EST 05-JUL-2001
DEFINITION 602907395F1 NCI_CGAP_K1d14 Mus musculus cDNA clone IMAGE:5064407
5', mRNA sequence.
ACCESSION BI143740
VERSION BI143740.1 GI:14603741
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 858)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs@email.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1173 row: n column: 24
High quality sequence stop: 854.
Location/Qualifiers
1. 858
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5064407"
/clone_lib="NCI_CGAP_K1d14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site: 1; Notf:
Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. 1"

FEATURES

source
BASE COUNT 227 a 220 c 201 g 210 t

Db 489 ACGGTTACCGCTGTGTACCGAAGAGTGTCTGTGTGCTGTACTGTACAGATGATCCTTCAGT 548
Qy 506 ccacttaagtgcatcataaatacttatacttgagagcttggtggtccaaataggca 555
Db 549 CCATCTCTGAGCTCATATTAACACCTTCATCTATGTGAGAGCGCTTGGCAAAATGGCAA 608
Qy 566 ctgcgtgaagaagagccaaacattcgttctagctacttctgcatatagatagag 625
Db 609 CTGCGCGGAAGAGAGCGCAGACCATACGCTTACGCTATTTTGGCCCTCATTTGATAGAG 668
Qy 626 atgggaagctt- gectcatgtggcgatgtgattcttcggccaaacacagtgtagaa 664
Db 669 ACGGAGAGCTTGTGCTGTGCTGCGCATATGATGATCGAACAACCATGTGTAGAG 728
Qy 685 ggaacagtagagcccaacttcgcgtat 714
Db 729 GGCACGGTGAAGCCCACTTCTGCGCTAT 758

RESULT 3
BF780854 710 bp mRNA linear EST 12-JAN-2001
DEFINITION 602105743p1 NCI-CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223626
5', mRNA sequence.
ACCESSION BF780854
VERSION BF780854
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 710)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9812 row: f column: 11
High quality sequence stop: 703.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223626"
/clone_11b="NCI-CGAP_Kid14"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library. 1"
BASE COUNT 198 a 177 c 177 g 158 t
ORIGIN

Query Match 30.2% Score 456.4 DB 10; Length 710;
Best Local Similarity 83.5% Pred. No. 8.6e-102;
Matches .552; Conservative 1; Mismatches 103; Indels 5; Gaps 3;

Qy 624 agatgggaagcttgcctcatgtgctgcatgtgtgatttctggccaacacagtgtaga 683
Db 1 AGAGGGGAGAGCTTGGCTCATGTGGCGCATAGTAGTCTCCGACCAACCATGTGTAGAG 60
Qy 684 aggaacagtagaacccaacttcctgcgtatatacagaagaacagtgaggagatgacat 743
Db 61 GGGACAGGTGAGGCCCACTTCTGCGCTATTCAGAAAGACAGTGAAGGAGGATGACGAT 120

Qy 744 ggcattaaagacctcaaatagtcagagaccacaaatcatccttgctgccccggttaactat 803
Db 121 GGGCTTTAAAGACCTCAAACTGCTCAATGACAGATAATCTGTTGATCTCACTGACTAT 180
Qy 804 tgcctatgaatgacatagagaccctctgta tgcctcttgaccggaagcaatagcaaa 863
Db 181 TGTCATGAATAATGACCATGAGAGCCCTGCTATGCGCTTGACCGCAAGSCATGGCCAA 240
Qy 864 agataacttgagatttggtgacattatctactgtgaltccacitggaacatctca 923
Db 241 AGATAATTTTCGAGATTCTGCTGACATTTATTTATCTGATGATTCACACTGGACATCCCA 300
Qy 924 ccaattagaagctcctaagttcccgaraaatctcctggggcactaggttaatatgt 983
Db 301 CCAGTCAGAGATTCTCTACATCCCGAGAAATTTCTGTGGGCCACAGGTTTATATATGT 360
Qy 984 ctggaagtltaagagagatlatcaaaagtgaactgcttatacagttgaaagagtlgga 1043
Db 361 ATTGGAAGTGAAGAGAAAGTACTACAAAGTGAAGTCACTCTTGCACTTTGAAGGAAGCTGCA 420
Qy 1044 agtataagcccccttggcagtgccaagaatlgagactggaagaccagagctccaca 1102
Db 421 AGCTACAGCCCTCTTGTGAGTCCAAACACTGAGCTGGAAGGACCAACTCAACAA 480
Qy 1103 --tagaaaagacacacacagttcgagaatctcgcagctggaacccaagcgagagag 1160
Db 481 CTTGGAAGAAACCTGCCCTGCGAGAGTCTGCAATTTGTGACCAACACCCAGAGCGG 540
Qy 1161 gtcattagtgacagtgccattgtgcagcagctggtgtaaacctctggagagaccacact 1220
Db 541 GTCTTCAGGGCAGTGTGCTGTGTGAGCAGCT- GTGAGAAACCAAGAGAGACCGTCTGT 599
Qy 1221 tgcgcacacatgatatagggaaacacactatcagaagctctccctgacttaacang 1280
Db 600 CCCCACAGATGATGATGAGAGATGCTCCATCAGAAAGCCCT- CCTGACTTTAATATAG 658
Qy 1281 a 1281
Db 659 A 659

RESULT 4
A1636030/c 606 bp mRNA linear EST 16-DEC-1999
LOCUS A1636030/c
DEFINITION t292a03.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296012 3'
similar to SW:IRRX_RAT P52191 INWARD RECTIFIER POTASSIUM CHANNEL
B1R9 ;, mRNA sequence.
ACCESSION A1636030
VERSION A1636030
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 606)
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
Unpublished (1997)
AUTHORS Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
[www-bio.llnl.gov/dbp/image/image.html](http://www.bio.llnl.gov/dbp/image/image.html)
Insert Length: 681 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 446.

Db	647	CTTGCCCGGAAGAGACGACACATTAACGCTTACAGTATTGGCCCTCTATGATAG	706
Qy	624	agatggaagccttgccatcattgtgcgcacattgtgatttcggcccaa	671
Db	707	AGACGCGAAG-TTTCCTCATGTGGGGAATGATGTAATTCGACCAAA	753
RESULT	6		
LOCUS	BI101237	662 bp	mRNA linear EST 26-JUN-2001
DEFINITION	602886939r1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042480		
ACCESSION	5', mRNA sequence.		
VERSION	BI101237		
KEYWORDS	BI101237.1 GI:14552130		
SOURCE	EST.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC). Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1AM1116 Row: m Column: 09 High quality sequence start: 24 High quality sequence stop: 660. Location/Qualifiers 1. 662 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:5042480" /clone_lib="NCI_CGAP_Kid14" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: kidney; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. "		
BASE COUNT	160 a 168 c 152 g 182 t		
ORIGIN			
Query Match	28.6%; Score 431.4; DB 10; Length 662;		
Best Local Similarity	83.3%; Pred. No. 1.2e-95;		
Matches 539; Conservative 0; Mismatches 101; Indels 7; Gaps 4;			
Qy	192	cattttggagaatgggaagctatgtgtgtacatcttcaccactctgtgagaccaa	251
Db	16	CACCTCTGGAGAAATGGGGAGCTACATGTTGATATTTTACCACCTCTGTGATACCA	75
Qy	252	gtggcgccatatgtttgtgatatcttcttatactatattctctcggtgtgatat	311
Db	76	GTGGGGCCATATGTTCAATATATTTTCTCTGTCTACATTCCTCTGCTGATATTTGG	135
Qy	312	ctctgctcttggctcatagccttcacatcatgagcatcattaaatgatacgacataac	371
Db	136	TTTCATATTTTGGCTCAATAGCCTTTCATCAGGAGACCTATTAGCGATCAGATATCAC	195
Qy	372	acctgtgtgtgacaacagctcattcttcaagaaggcctttgtctcctctagaccaa	431
Db	196	CCCTTGTGTGACACGATGATTTTACATGAGCTGATTTTATTTCTCCTGTGAGACCA	255
Qy	432	aaccacacatagatatggttatacgtctgtgttactgaagaatgtctctgtgacggtcat	491

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	256	GAACACCATGGATACGGTTACCGCTGTGTACCGAAGAGTCTGTGTGCTGTACTAC						
Qy	492	ggtgtaacctccagatcatttaagtgtgatacaataatcattatcatgtagagctgctt						
Db	316	ACTGATCCCTTCAGTCCATCTCAGCTGCATCATTAACACCTTCATCATTTGAGACAGCTT						
Qy	552	ggcccaa-atggcaactgctcgaagaagaccacaacattcgcttgcacttgcaac						
Db	376	GGCCAAAGATGGCAACTGCCCGGAAGACAGCCCAACACATACGCTTACGATATTTGGCC						
Qy	611	ttataggatagaga--gattggaacattgctcctatgtggagcatgtgatttcggcc						
Db	436	TCATTGGATGTGAGACAGCGGAACCTTTGCTCTCATGTGGCCCATAGGTGACTTCCGACC						
Qy	669	aaacacactgtgtagaagaacagcttagag---cccaactctccgctatacagaagacag						
Db	496	AAACCATGTGCTCAAGAGGGCAGCTGTGACAGGCCCACTTCTGGCCATTTCAAGAACAG						
Qy	726	tgaaggagagatgacatgagcatlta-aagacctaaattgltcaagacaaatcatcc						
Db	556	TCACGGGAGGAGATGACGATGGCGCTTACAAAGACCTCAAACTCGTCAATGACGATATCC						
Qy	785	tgttaccoccgtaactatgtcctatggaatgaccatgagagccct						
Db	616	TGTGACTCTCAGTGAATGTGCTCATGACATTGACCATGAGAGAGCCCT						
RESULT	7							
LOCUS	BI101492	686 bp	musculus	linear	EST	26-JUN-2001		
DEFINITION	602887284F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5042372							
ACCESSION	BI101492							
VERSION	BI101492.1	GI:14552385						
KEYWORDS	EST.							
SOURCE	house mouse.							
ORGANISM	Mus musculus							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
TITLE	1 (bases 1 to 686)							
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgabbs-remail.nih.gov							
	Tissue Procurement: Jeffrey E. Green, M.D.							
	cDNA Library Preparation: Life Technologies, Inc.							
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LMNL at:							
	http://image.lnl.gov							
	Plate: LM11116 row: h column: 21							
	High quality sequence stop: 684.							
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	/db_xref="taxon:10090"							
	/clone="IMAGE:5042372"							
	/clone_id="NCI_CGAP_Kid14"							
	/lab_host="DH10B (T1 phage-resistant)"							
	/note="Organ: kidney; Vector: pCMV-SPO6; Site_1: NotI;							
	Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.							
	Average insert size 1.75 kb. Constructed by Life							
	Technologies. Note: this is a NCI_CGAP Library."							
BASE COUNT	194 a 155 c 150 g 187 t							
ORIGIN								
Query Match	28.5%, Score 429.4, DB 10, Length 686;							
Best Local Similarity	83.5%, Pred. No. 3.8e-95;							

Matches	487	Conservative	0	Mismatches	96	Indels	0	Gaps	0
Qy	26	ccctaaggacaagcaagaatagactatlaagcgagcgactatataatlaatcaatgcgg	85						
Db	89	ccctTAAGGACCAAAAGAAAGAAAGACTATTACGGAAGTAGTCACAGGATGTCAATGTGG	148						
Qy	86	acgcaaatataccaggctacaccccgacagacacattatagctgagaagagaagaaga	145						
Db	149	ACTCCAANATATCCAGGCTATCTCCAGACATGCCATCGCTAGAAAGAAAGACAGAGA	208						
Qy	146	gacgaattacttacaagaatgagcagctgtaatgcttaacttcaagacatlttggagaat	205						
Db	209	GGCGGTTGATCCACAAAGATGCGACACTGTAAAGTGTACTTTAAACATTTTGGAGAA	268						
Qy	206	ggggagacatgtagttagacatcttcaacacactctgtgagacaagaagtgagcatalgt	265						
Db	269	GGGGAGAGCTACATGTTGATATTTTACACACTTGTGGATACCAAGTGCCCATATAT	328						
Qy	266	ttgtgatatlttcttatctatatactctcgtggttggatatltgtctgtcttcttggc	325						
Db	329	TCATATATATTTCTGCTGTCTTACATTTCTCTCGTGTGATATTTGGTCCATATTTAGC	388						
Qy	326	tatagccttctatcatgycgcatctataaagatccagacatacacttgttgttgaca	385						
Db	389	TCATAGGCTTTATATACGGAGACTATTAAAGGATTCACAGATATACACCCCTTGTTGACA	448						
Qy	386	acgtcacctcttccacaaggcgcccttctctcccttaagacccaacaacacataagat	445						
Db	449	ACGTGATTCATTTACGGCTGATTTTATCTCCCTGGAGACCAGACACACATTTGAT	508						
Qy	446	atggtatctgcgtgttactgaagaatgtctgtggccgtgctcatgltgactccatg	505						
Db	509	ACGGTTACCGCTGTGTACACGGAAGTGTCTGTGTGCTGTACTGTGACAGTATCTTTCAT	568						
Qy	506	ccatcttaagttgcacataaataactctatataattggagctccttggccaataatggcaa	565						
Db	569	CCATCTCAGCTGCATCATTAACACCTTATATTTGGACGACGAGCTTTGGCAAGATGGCA	628						
Qy	566	ctgctctgaagaagagcccaaacattcglttcaagctacttgc	608						
Db	629	CTGCCCGAAGAGAGCCAGACCATATACGCTTCAGCTATATATGCG	671						
RESULT	8								
LOCUS	AM475637	721 bp	linear	EST 24-FEB-2000					
DEFINITION	un99d09.y1 Sugano mouse kidney mR1a mus musculus cDNA clone								
IMAGE	5520017.5	similar to	TF:Q92307	Q92307	IMWARDLY RECTIFYING				
POTASSIUM CHANNEL KIR5.1					mRNA sequence.				
ACCESSION	AM475637								
VERSION	AM475637.1	GI:7045743							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
	1 (bases 1 to 721)								
	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,								
	Underwood,K., Steptoe,M., Theisling,B., Allen,M., Bowers,T., Person								
	,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter								
	,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,								
	Waterston,R. and Wilson,R.								
	The Washon-NCI Mouse EST Project 1999								
	Unpublished (1999)								
	Contact: Marra M/Washon-NCI Mouse EST Project 1999								
	Washington University School of Medicine								
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA								

```
Trace considered overall poor quality
Seq primer: custom primer used
High quality sequence stop: 1.
      Location/Qualifiers
          1. .721
FEATURES
    source
```

BASE COUNT	sequencing: 5' end primer CTTCTGCTCTTAAACCTCG and 3' end primer CGACCTGCAGCTCGACACA."			
ORIGIN	208 a	176 c	179 g	158 t

Query Match	Similarity	26.6%	Score	401	DB	9	Length	721
Best Local	Similarity	75.8%	Prod	No.	3	9e-88		
Matches	521	Conservative	1	Mismatches	161	Indels	4	Gaps
QY	582	ccaaccatcgtcttcagctactcttgcaactataggtatgagagatgaggaaagcttgacct	641					
DB	1	ccacaccatagcgttgagctatataatagccgcattctggggatagtgaccggatcgctgctt	60					
QY	642	catgtgagcgcatcttggaattcttggcccaaccacggtgtagaaagaaacgttaagccca	701					
DB	61	catgtggggcctatgagatcttccgacacaaacatgtgggggaagcgacagtbaagacc	120					
QY	702	actctccgcctacagaaagacagtgaagaagatgaacatgacatgtcaatttaaaagacctaa	761					
DB	121	acttatggcgctatttcacaaagacatgaaaggaagagatgacattggcgtttaaagacctca	180					
QY	762	atcagtaacagcaacaatcabcctgctgtaccccggttaactatgtccatgtaaatgcaca	821					
DB	181	actctctcagtcacacagatamgacctgggtactctccaggagactattgttcataaataagacca	240					
QY	822	tgaagagccctctgtatctcccttcacgcgcaagacagtagcccaagaataacttggagattt	881					
DB	241	tgagagcccttggatagtcgcctggaccccaagcgaagctggcccaaaagatatttaccagagctt	300					
QY	882	ggtgcacatttactatactgctgtgatttccacttggaaacatctcacaactcagaagctccta	941					
DB	301	ggtgacatatattatattactggtgatttccacttggagacatccacacagctccagaattccta	360					
QY	942	tgctccccgaaatctctctgggggcataaggttaatatgctcttggaaagttaagaagaa	1001					
DB	361	catccccagaaataattctctggggccacagagtttctatgatagtttggaagtgaagaa	420					
QY	1002	gtatacaaaagtgaacgctctacaggtttgaagaagatgttggaaatgatctgccccctttg	1061					
DB	421	gtactacaaagtgaaactgctttggcattgttgaagaaagacagggaaattttacgccccctttgg	480					
QY	1062	cagttgccaaagcaatctggaatgaagaacagcagctccaca---tagaaaagcaaccac	1116					
DB	481	cagtgcccaaacacttgagactgtatagaccgcacgaacgctcaactttgaamaaaaacgncgc	540					
QY	1119	agcttgagaaatccctgcacgcttcgagacaccaaagcgagaaagaaagtcatcttagtgcagttgc	1177					
DB	541	tgccccgagatcttcapaaattttgcacacacacacacacacattgattctcccttaagggcacaatttgc	600					

QY	1179	catcttcagcagcacttggtgaagacccctggagaccacacacttgcgcacacatgaata	1238
Db	601	CGTGGTGAACACCT-GTGAAGAACCATATGACGATGCAGCTGTCCACACAGATGATGTG	659
QY	1239	gggaacacacctatcagaagaactctc	1265
Db	660	AAGATATGCTCTATCAGATATCATCTGC	686
RESULT	9		
BF789666		783 bp	mRNA
LOCUS			linear
DEFINITION			EST 12-JAN-2001
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
BASE COUNT			
ORIGIN			

[illegible]

BR411612/c	RESULT 10
LOCUS	BF411612 516 bp mRNA linear EST 28-NOV-2000
DEFINITION	UI-R-BT1-bmp-d-10-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
ACCESSION	BF411612
VERSION	BF411612.1 GI:11399601
KEYWORDS	EST.
SOURCE	Notway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Enkayrta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE	Rattus.
JOURNAL	1 (bases 1 to 516)
MEDLINE	Bonaldo,M.F., Lennon,G. and Soares,M.B.
COMMENT	Normalization and subtraction: two approaches to facilitate gene discovery
	Genome Res. 6 (9), 791-806 (1996)
	9704447
	Contact: Soares, MB
	Program for Rat Gene Discovery and Mapping
	University of Iowa
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA
	Tel: 319 335 8250
	Fax: 319 335 9565
	Email: msoares@blue.weeg.uiowa.edu
	The sequence contains an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a donatide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized mid-brain library cDNA library preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics (www.resgen.com)
	Seq primer: M13 Forward
	POLYA=yes.

	Query Match	24.8%	Score 374.8	DB 10	Length 783	
	Best Local Similarity	79.3%	Pred. No. 1.1e-81			
	Matches	520	Conservative	0	Mismatches	127
					Indels	9
					Gaps	6
Oy	26	cctaaggagcacaagaatgagtctatacgacgcagctatcatatcaatgcgg	85			
Dd	127	ccctTAAGGACCAAAAGAATGACCCTTTACGGAAAGTACTACAGATTGTGCATGTGG	186			
Oy	86	acgcaaaatacccaggtaccgccagagcacattatagcttgagaagaagaagcaaa	145			
Dd	187	ACTCCAAATATTCACAGCATCTCCACAGAGCATGTCATCGTCAGAAAGAACACAAATAA	246			
Oy	146	gacgaacttccaagaatgcaacttaatgcttactcttaagaacatttttgaagat	205			
Dd	247	GCGCCTTCTCCACAAAATGGCACCTTAATGTGTACTTTAAACAATTTTTGGAGAT	306			
Oy	206	ggggaagctatgtggttagacatcttcaccacctctgttgaaaccaagtgycgcacatgct	265			
Dd	307	GGGGAGCTACATGTTGATATTTTACCACGCTTGTSGATATCCAAGTGGGCCCATATGT	366			

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FEATURES
source
Location/Qualifiers
1. 516
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/cd_xref="taxon:10116"
/clone="UI-R-BT1_bmp-d-10-0-UI"
/clone_1b="UI-R-BT1"
/dev_stage="adult"
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OY	206	gggagagatgtagtggcttgaacacatccacacactctgtgaaagccaaagtgagggccataatgt	265
Db	332	ggggagagcttaccatggcttgaatatt	391
OY	266	ctgtgataatcttcttatacctataatctctcgtgtgtgataattggctctgtctctttggc	325
Db	392	tctgtaatt	451
OY	326	tcaatagccttcaatcatatgagcgaactatttaaaatgacacagacactcaactctgtgttgaca	385
Db	452	tcattatggccttttcattacggagacactatttttaaggagatccagattttcacccttctgttgaca	511
OY	386	acgttcacattcttccacagagggccctttttgtctctccctagagaagcccaaacaccataagat	445
Db	512	acgttcacatttcattttacggcctgcatttttttttttttttttttttttttttttttttttttt	571
OY	446	atggtctatcgcctgttctactgaagaatcttctgtgacgctgtctcatgtgtatgcctccaat	505
Db	572	acggttaccgcctggcgctacccgaaagagctctgtggggcctgtactgacccggagatcccttagt	631
OY	506	ccactctaaag	515
Db	632	ccatctcttag	641

RESULT	13
BF789809	665 bp mRNA
LOCUS	linear
DEFINITION	602105362n1 NCLCGAP_kid14 Mus musculus cdna clone IMAGE:4223350
	5', mRNA sequence.

VERSION	BF789809.1	GI:12094845
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 665)

NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg Ph.D.

Email: cgabps.r@mail.nih.gov
Tissue Procurement: [jeffrey.E.Green, M.D.](mailto:jeffrey.E.Green@M.D.CDNA.Library.Preparation@LifeTechnologies.Inc)
CDNA Library Preparation: [Life Technologies, Inc.](mailto:LifeTechnologies.Inc.CDNA.Library.Preparation@LifeTechnologies.Inc)
CDNA Library Arrayed by: [The I.M.A.G.E. Consortium \(LNL\)](mailto:TheI.M.A.G.E.Consortium@LNL)
DNA Sequencing by: [Incyte Genomics, Inc.](mailto:IncyteGenomics.Inc)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
plate: LLM8811 row: 1 column: 15
High quality sequence stop: 617.

FEATURES	Location/Qualifiers
source	1. .665

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223390"
/clone_1lb="NCLCGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-SpOr6; Site:1: NotI;
Site:2: SalI; cloned unidirectionally. Primer: oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCLCGAP Library. I"

```

Query Match	23.4%;	Score 353.8;	DB 10;	Length 665;
Best Local Similarity	82.4%;	Pred. No. 1.6e-76;		
Matches 453; Conservative	0;	Mismatches 93;	Indels 4;	Gaps 4

Oy	26	cccttaagggaagaagaagaatgaaccttaacgaagaagatcatatcaatctgaagc	85
Db	101	CCCTTAAGGACCAGAAAGATGAGCTTTACGGAAGTAGCTACAGAGATTGTCAATCTGG	160
Oy	86	acgcaaaataccgaagctacccgcagagacatatagctltgaagaagaagaagaa	145
Db	161	ACTCCAAATATTCAGAGCTATCTCCAGAGACATGCGATCGTGAGAAAGAGCAGAA	220
Oy	146	gaagatctaccacaagaatgagcagctgaatgcttacttcaagaacatttttgaagat	205
Db	221	GGCGGTTCTCCACAAAGATGGCACCTGTAATGTCTACTTTAAACATTTTGGAGAT	280
Oy	206	gggaagaactaigtgttgacatcttcacacactcttggaaaccaagaaggcgcaatgt	265
Db	281	GGGGAGGCTACAGTGTTATATTTTACCACCTCTTGTSATACCAAGTGGCCCATATGT	340
Oy	266	ttgtgatatcttcttatactatactctcgtgtgtgatatattgctctgtctttggc	325
Db	341	TCATATATTTTCTGTGCTTACATTTCTCTCGTGATATTGGTTCCATATTTTGGC	400
Oy	326	tcaatgaccttcatactgagatcctataataatgatccagacatcacacctgtgttgca	385
Db	401	TCATGACGCTTTCATCACGAGACGACATTAAGGATCCAGAAATCAACCCCTGTG-TGCA	459
Oy	386	acgtccactcttctcaaggggcccttttggcttccctccatagaaccaaacacaaatagat	445
Db	460	ACGTCAATTCATTTTACGGCTGCATTTTATTTCTCCCTGAGACCCAGCACACCAATGGAT	519
Oy	446	atggtcatcgctgtgttactgaagaatgtctctgtgacgctgtca-tgttgatccctcag	504
Db	520	ACGGTTACCGGCTGTCAACGAGAGTGCTGTGTGGTGTACTGACAGNTGATCCTTCAG	579
Oy	505	tccatcttaagttgcatcataataaacttlatcatttggagctgctgtggccaatatggca	564
Db	580	TCCATCCTCTCAG-TGCATCATAAA-ACCTTCATCATTTGAGCGACGCGCTGGGAAAAATGGGC	637
Oy	565	actgtcgaa 574	
Db	638	ATGGCCCGAA 647	

RESULT	14
LOCUS	AQ222870
DEFINITION	AQ222870 461 bp DNA linear GSS 19-SEP-1998
ACCESSION	HS_2014_2-H08_MR CIT Approved Human Genomic Spectrum Library D Homo sapiens genomic clone Plate=2014 Col=16 Row=0, DNA sequence.
VERSION	AQ222870
KEYWORDS	AQ222870.1 GI:3636483
SOURCE	GSS.
ORGANISM	human.
	Homo sapiens

REFERENCE
AUTHORS

1 (bases 1 to 461)

Euarchyota; Metazoa; Chordata; Crinacea; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

Mañanías, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE	Sequence-tagged connectors: A sequence approach to mapping
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT	scanning the human genome
LINE	99380589
CONTACT	Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2014 ROW: 0 Column: 16
Class: BAC ends
High quality sequence stop: 461

FEATURES

Location/Qualifiers


```

source
1. 461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate2014 Col=16 Row=0"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT      136 a      102 c      106 g      117 t
ORIGIN

Query Match      22.6%; Score 340.6; DB 12; Length 461;
Best Local Similarity 96.7%; Pred. No. 2.7e-73;
Matches 357; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 637 tgcctatgtgcgcattgtgatttcggccaaccagtgtagaaggaacagttaga 656
DB 2 TGCCTATGTGGCGCATGTGTGATGTGCGCCAAACACCTTGTAGAGAACAGTTAGA 61

QY 697 gcccaacttcgcctatcacagaagacagtgaggagagatgcagtgcatttaagac 756
DB 62 GCCCACTTCTCGCTATACATAGACAGTGAAGGAGATGACATGGCATTTAAGAC 121

QY 757 ctcaaatagtcacagcaacaatcactcgtgtcaccccgtaactatgttcatagaat 816
DB 122 CTCGAATATATCAACGACCAAAATCATTTGTGTCACCCCGGAACATTTGCCATGAAT 181

QY 817 gacacatgagagccctctgtatgccttcgacgcgaagacagtagccaaagaattag 876
DB 182 GACCATGAGAGCCCTCTGTATGCTTGAACCCGATAGCAGTATCAAGTAACCTTGAG 241

QY 877 atttgtagacattatcactatgtgtgatttcacatgcgaacatcaccatcagaagc 936
DB 242 ACTTGTGTCATATTTATCTATAGTGTGATTCACATGGAACATCTACCATTAAGAC 301

QY 937 tccatgttcccccagaaatctctcgtgggcccagaagtttaataatgtcttgaaatag 956
DB 302 TCCATATGTTCCCGAGAAATTTCTGTGAGCCATAGGTTATATGATGTCTTGAAG- 360
TAAG 360

QY 997 aggaagat 1005
DB 361 AGGAAGTAT 369

RESULT 15
BF194884/c 527 bp mRNA linear EST 03-NOV-2000
LOCUS BF194884
DEFINITION 7089h02.x1 NCI-CGAP Kid11 Homo sapiens cDNA clone IMAGE:3643634 3'
similar to TR:092307 Q92307 INWARDLY RECTIFYING POTASSIUM CHANNEL
KIR5.1; mRNA sequence.
ACCESSION BF194884
VERSION BF194884.1 GI:11081177
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 527)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov

```

```

FEATURES          High quality sequence stop: 475.
Location/Qualifiers
source
1. 527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3643634"
/clone_lib="NCI-CGAP Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker. Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502853). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT      162 a      106 c      93 g      166 t
ORIGIN

Query Match      21.9%; Score 330; DB 10; Length 527;
Best Local Similarity 95.3%; Pred. No. 1.1e-70;
Matches 382; Conservative 1; Mismatches 12; Indels 6; Gaps 4;

QY 1108 aagcccccacagttcgaatctcgcagtcgacaccaaagcgagagagttcat 1167
DB 527 AAAGCACACCACTTGAGATCTGCTGACGACACCAAGCGAGACCAAGTCATTT 468

QY 1168 agtgcagttgccattgcagcagctgtgaaacccctgagagacacacacttcgca 1227
DB 467 AGTGCAGTTGCCATTGTGACGACCT-GTGAACACCTGAGAGACCAACCACTTCCGCCAC 409

QY 1228 acatgaatagggaaacacacttataagaagctctccctgactttaacangaatcctc 1287
DB 408 ACATGAATATAGGGAACACCTTATGAGAAAGCTCT-CTGACTTTAAACAG--AATCTC 352

QY 1288 tgtwgaatcccaatgttagtccctaaatgtcaattatgagggctaccactgatact 1347
DB 351 TGTAGATCCCAATGT--AGTCTTAATTGCAATTTAGAGGCTACCACTGATATTT 294

QY 1348 tatcttcagccaatcaagtcgtgtgaaacgttcttcttgaaagtgtatgctatgt 1407
DB 293 TATCTTTCAGCCAAATCAAGTCGTGTAACGTGTGCTTTTGAAGGTATGCTATGT 234

QY 1408 ttatgatgatgtcgtggttagtagtagtaacttggtlaaagataatcctaaat 1467
DB 233 TTTATGATGATGCTGCGGTAAGTAGAGTAACTTGTAAAGATATATTAATAATT 174

QY 1468 ccatagttccagttatataaatttctgttcgggaatt 1508
DB 173 CCATAGTTCACGTATTAATAATTTTCTTGTGCGCAATT 133

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Search completed: October 5, 2002, 03:59:14
Job time: 8929 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 02:43:00 ; Search time 53.33 Seconds
(without alignments)
6950.327 Million cell updates/sec

Title: US-09-623-304A-2
Perfect score: 1509
Sequence: 1 ttactactacaacacc.....ttttctgttcggaattc 1509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfilist1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280.4	18.6	2310	1	US-08-461-690B-1
2	280.4	18.6	2311	1	US-08-103-445-1
3	182	12.1	1260	1	US-08-385-186-1
4	181.8	12.0	1245	1	US-08-385-186-14
5	176.4	11.7	1095	1	US-08-385-186-8
6	176.4	11.7	1425	1	US-08-385-186-12
7	172.8	11.5	1978	1	US-08-614-801A-3
8	172	11.4	1260	1	US-08-385-186-3
9	167.2	11.1	1827	1	US-08-103-445-3
10	167.2	11.1	1827	1	US-08-461-690B-3
11	165.6	11.0	2070	1	US-08-486-342-1
12	165.6	11.0	2070	1	US-08-473-092-1
13	165.6	11.0	2070	1	US-08-614-801A-1
14	165.6	11.0	2076	1	US-08-066-371-1
15	165.6	11.0	2076	4	US-09-042-494-1
16	165.6	11.0	2076	5	PCT-US94-05666-1
17	159.6	10.6	2301	1	US-08-614-801A-5
18	155.6	10.3	2896	2	US-08-709-923-1
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31	138.8	9.2	1119	2	US-08-501-003A-8	Sequence 8, App11
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34	138.8	9.2	1591	2	US-08-501-003A-5	Sequence 5, App11
35	138.8	9.2	1591	5	PCT-US94-01210-5	Sequence 5, App11
36	138.8	9.2	1671	2	US-08-501-003A-3	Sequence 3, App11
37	138.8	9.2	1671	5	PCT-US94-01210-3	Sequence 3, App11
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44	32.4	2.1	5994	3	US-09-032-365A-11	Sequence 11, App1
45	31.8	2.1	1273	4	US-09-319-892-3	Sequence 3, App11

ALIGNMENTS

RESULT 1
; Sequence 1, Application US/08461690B
; Patent No. 5670335
; GENERAL INFORMATION:
; APPLICANT: Jan, Lily Y.
; APPLICANT: Jan, Yuh Nung
; APPLICANT: Kubo, Yoshihiro
; APPLICANT: Reuveny, Eitan
; APPLICANT: Slesinger, Paul A.
; TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
; TITLE OF INVENTION: Potassium Channel cDNAs
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,690B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,445
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreyer, Walter H.
; REGISTRATION NUMBER: 24,190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2310 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 338..1624

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US-08-461-690B-1

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Query Match      18.6%; Score 280.4; DB 1: Length 2310;
Best Local Similarity 57.5%; Pred. No. 6.4e-76;
Matches 569; Conservative 1; Mismatches 402; Indels 18; Gaps 3;

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RESULT 2
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Sequence 1, Application US/08103445
Patent No. 5492825
GENERAL INFORMATION:
APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yuh Nung
APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan
APPLICANT: Siesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
NUMBER OF INVENTIONS: 26
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco,
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,445
FILING DATE: 06-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 338..1624
FEATURE:
NAME/KEY: misc_feature
LOCATION: 596..661

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OTHER INFORMATION: /note="Region encoding M1
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US-08-103-445-1
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Best Local Similarity 57.5%: Pred. No. 6.4e-76;
Matches 369: Conservative 1: Mismatches 402: Indels 18: Gaps 3:
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RESULT 3
US-08-385-186-1
; Sequence 1, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P
; APPLICANT: Ashford, Michael J
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Steuart Street tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION: 435
; PRIORITY INFORMATION:
; APPLICATION DATA:
; FILING DATE: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 14210-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
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; NAME/KEY: misc.feature
; LOCATION: 1..1260
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; OTHER INFORMATION: ATP-sensitive potassium channel protein."
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US-08-385-186-1

Query Match 12.1%; Score 182; DB 1; Length 1260;
Best Local Similarity 52.9%; Pred. No. 6.5e-46;
Matches 470; Conservative 1; Mismatches 396; Indels 21; Gaps 3;

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DB 635 acgagaaagctgtgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 694
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QY 686 gaacagctgaagacccaacacacacacacacacacacacacacacacacacacac 742
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DB 695 cctccatccggggcacaagctcattcattcattcattcattcattcattcattcatt 754
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QY 743 tggcatttaagaacctcaaatag-----tcaagacccaatcattcattcatt 790
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DB 755 tgaaccagacacacacacacacacacacacacacacacacacacacacacacac 814
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QY 791 ccccgtaactatttctcattgaatattgacacagagagacacacacacacacacac 850
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DB 815 ctccctctgtatcttctccacagatcacaagagagacacacacacacacacacac 874
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QY 851 aagcagtaagcaaaataactatgagattgtgacattatctatctatctatctatct 910
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DB 995 gatctcaccacacacacacacacacacacacacacacacacacacacacacac 1054
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QY 1031 aaggaagtgtagaagatataatgcccccttctgacgtgacgaagaattgtg 1078
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DB 1055 atgatatcctatagacacacacacacacacacacacacacacacacacacac 1102
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RESULT 4
US-08-385-186-14
; Sequence 14, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:

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APPLICANT: Adelman, John P
APPLICANT: Ashford, Michael J
APPLICANT: Bond, Chris T
TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,186
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ. ID NO. 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 22..1242
OTHER INFORMATION: /note= "Encodes a full-length or
OTHER INFORMATION: nearly full-length human pancreatic beta cell
OTHER INFORMATION: ATP-sensitive potassium channel protein: Seq ID.
OTHER INFORMATION: 15."
US-08-385-186-14

Query Match 12.0%; Score 181.8; DB 1; Length 1245;
Best Local Similarity 52.7%; Pred. No. 7.5e-46;
Matches 474; Conservative 1; Mismatches 403; Indels 21; Gaps 3;

QY 212 gctatgtgttgacatctaccacactctgtgagacccaagtcgacatattgtga 271
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DB 197 gctacctgacacacacacacacacacacacacacacacacacacacacacacac 256
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QY 272 tatttcttatactatattctctgtgtgtatatttgctctgtcttggctcattg 331
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DB 257 tttttgtcatgttttaccagatgacacacacacacacacacacacacacacacac 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 ccttcatatagcgatctat-----taagatccagacacacacacacacacattgt 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 317 catatcatgagggagacacacacacacacacacacacacacacacacacacacac 376
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QY 386 acgtccatctcttcacaaagggcccttcttccctagagacccaacacacacatgat 445
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DB 377 acctcaacgggttctgtctgtcttcttcttcttcttcttcttcttcttcttctt 436
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QY 446 atggtatcgcgtgcttactgaagaatgtctctgagccgctcattggtatccaccagt 505
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DB 437 ATGGCTACCGGGGTCATACAGATAAATGCCCGAGGGAATTTCTTCTTATCCAAT 496
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 506 ccaatcttaagtctcatcaataaacttcaatcattgagctgccttggccaataggcaa 555
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DB 497 CTGTGTTGGGGTCATGTCAATGCATTCATGCGATGCATGTGTGTAATAATCTCTC 556
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 566 ctgctgagaagaagcccaaacatcgtcttcagctacttgcactatagatagag 625
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DB 557 AACCCAGAAAGAGAGGAGAGACCTGTCTTTCACACCAATGAGATGATCCATGGGG 616
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QY 626 atggagaagcttgcctcatctgagcagatggtgatcttcgccaacaacagtgtaag 685
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QY 686 gaacagttagaagcccaactctccgctatacagaagaagcagtgaggagg---atgacga 742
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DB 677 CTTCATCAAGAGCCAAAGTTGATCAAAATCCAAACAGACCTGGAGGGGAGCTTCATCCCGT 736
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DB 857 CCCAGCTGCCAAAGAGGAATGGAATGTGTGATCTCTAGAAGAAATGCTGGAAGCCA 916
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QY 911 ctggaacatcccaaatctagaagctcctatgtcccccgaaraattctctgggacata 970
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DB 917 CAGGGATGACATCCCAAGCTCGAAGCTCTACATCAACCACTGATCTCTGGGGTTACC 976
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QY 971 ggttaatgagtctcttgaagaagtaagaagatatacaagaagtaactgcttcaagttg 1030
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DB 977 GGTTCACACCTGCTCTGACCTCGAGAGCGGTTCTAGCAAGTTGATCAACAGCTTCC 1036
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QY 1031 aaggagaagtgtgagaatatatgcccccttctgcagtcgccaagaacttggactgaaagac 1089
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DB 1037 ATGAGACTATGAGACCAACGACCCCATCCCTTAGTGCCCAAAAGAGCTGGCGAGTTAGCC 1095
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APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1095
OTHER INFORMATION: /note="Sequence of cDNA clone
Patent No. 5744594
OTHER INFORMATION: encoding a portion of rat pancreatic beta-cell
OTHER INFORMATION: ATP-sensitive potassium channel protein."
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1092
US-08-385-186-8

Query Match      11.7%; Score 176.4; DB 1; Length 1095;
Best Local Similarity 51.8%; Pred. No. 3.2e-44;
Matches 461; Conservative 1; Mismatches 407; Indels 21; Gaps 2;

QY 212 gctatggttgacatcttccaccactctgttgagaccacgaagtgagccatagtgtgta 271
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DB 47 GATACCTGACGACATCTTACACCCCTGTGAGACTTAAGTGAGATTCACACTATTGA 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 272 tatctcttattatattctctcgtgtgttgatattgtgctcgtcttggcctatag 331
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 332 ccttcatcatgagcagatcat-----taaatgatacagacatcaacacttgtgtgaca 385
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 167 CATACATCCGGGAGATATGAGACACATAGAGAGAGACCCCGGTGAGACTCCCTGGTTACA 226
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 386 agtcatcattcttaagaaggccttcttctccctagaagacccaacacacatagat 445
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DB 227 ACCTCAACGGGTTGTCTCCGCTTTTATTTCTCATTAAGACAGAAACACCATTTGGTT 286
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QY 506 ccaatcttaagtctcatcaataaacttcaatcattgagctgccttggccaataggcaa 565
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Qy 626 atgggaagcttgcctcatatgagcgcattgtgatttcggccaacacagtgaggaag 685
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Qy 686 gaacagttagagcccaacttccgcctatacagaagaagaggaagagagat----- 737
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Db 527 CCTCCATGAGCCAGATTGATCAAGTCCAAAGACACTTCAGAGGGGAGTTCATCCCC 586
Qy 738 -----gacgatgcatltaagaacctcaattagtcacagcaaatcctcgtgta 790
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Qy 791 ccccgtaactatgtccatgaatgaattgacacagagagccctctgatacgccctgacgca 850
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Qy 851 aagcagtgcccaagataactttagatattgtgagacattatcctacactgtgattcca 910
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Qy 911 ctggaacatcacaacatcagaagctcctatgttcccgaraaatctctcgtgagccata 970
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Qy 971 ggttaatgatgtcttgaagttgaagaaagtattacaagtgaaactgcttacaagttg 1030
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Qy 1031 aaggaagtgtagaagtatatatgccccttgcagtgacgaagaagattgagc 1080
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RESULT 6

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US-08-385-186-12
: Sequence 12, Application US/08385186
: Patent No. 5744594
:
: GENERAL INFORMATION:
: APPLICANT: Adelman, John P
: APPLICANT: Ashford, Michael J
: APPLICANT: Bond, Chris T
: TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
: TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: Stewart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/385,186
: FILING DATE: 07-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/288,510
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/193,372
: FILING DATE: 08-FEB-1994
: ATORNEY/AGENT INFORMATION:
: NAME: Kruse, No. 5744594man J.
: REGISTRATION NUMBER: 35,235
: REFERENCE/DOCKET NUMBER: 14210-2-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 543-9600
: TELEFAX: (415) 543-5043

```

```

: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1425 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 56..1330
: NAME/KEY: misc feature
: LOCATION: 1..1425
: OTHER INFORMATION: /note="Encodes rat pancreatic beta
: OTHER INFORMATION: cell ATP-sensitive potassium channel protein."
US-08-385-186-12

Query Match      11.7% Score 176.4; DB 1; Length 1425;
Best Local Similarity 51.8%; Pred. No. 3.6e-44;
Matches 461; Conservative 1; Mismatches 407; Indels 21; Gaps 2;

Qy 212 gctatgtgtgacatcttcaacactctgtggaacacgaatgagccatagtttgta 271
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Db 285 CATACCTACGAGACATCTTTCACACACCTGGTGACCTAAAGTGAAGATTCACCTATTGA 344
Qy 272 tatttcttatactataatctctcgttggtgataattgtgctcgtcttctgtgctatag 331
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Qy 332 ccttcaatcagtgagatctat-----taatgatccagacatcacactgtgtgtgca 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 386 agctcattcttcaacagggcccttctgtctccctagagacccaacacatagag 445
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Qy 446 atggtatcgtcgtgtgtactgaagaagtctgtgagccgtgctcagtgatcctcagc 505
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Db 525 ATGGCTACAGGGGTCACTACGAGACAGTCCCGAGAGGATCATCTCCCTTAAATCCAGT 584
Qy 506 ccatttaagtgtcatataaataacttatactatgtagagcgtgccttgcgaataatgcaa 565
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Db 585 CCGTGTGGGTCATTGTCACAGCGCTTCATGATGATGATGATGATGATGATGATGATGATG 644
Qy 566 ctgctgaagaagagcccaacacatctgttcaagtaacttgcacttataagtagagag 625
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Qy 626 atgggaagcttgcctcatatgagcgcattgtgatttcggccaacacagtgaggaag 685
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Qy 686 gaacagttagagcccaacttccgcctatacagaagaagaggaagagagat----- 737
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Qy 738 -----gacgatgcatltaagaacctcaattagtcacagcaaatcctcgtgta 790
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Db 1005 CAGGAATGAGCTGCAAGCTCGAAGCTCTACGTACACAGTGAATGATCTGTGGGTTAC 1064

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,186
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/288,510
FILING DATE: 10-AUG-1994
APPLICATION NUMBER: US 08/193,372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1260
OTHER INFORMATION: /note="cDNA for rat heart
FEATURE:
NAME/KEY: ATP-sensitive potassium channel protein."
LOCATION: 1..1257
NAME/KEY: primer_bind
LOCATION: 472..491
OTHER INFORMATION: /note="Sequence corresponding to
Patent No. 5744594
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FEATURE:
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LOCATION: 632..651
OTHER INFORMATION: /note="Sequence complementary to
Patent No. 5744594
OTHER INFORMATION: Seq. I.D. No. 5744594.6"
US-08-385-186-3

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Query Match      11.4% Score 172; DB 1; Length 1260;
Best Local Similarity 51.2%; Pred. No. 7.6e-43;
Matches 465; Conservative 1; Mismatches 421; Indels 21; Gaps 2;

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QY 192 catttttggaatggaggaagctatgtgtgacacatcttaccactctgttgacacaa 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 CAATGTGAGGAACCTACGCTTACCTAGTACCTCTTACACACCTGTGTGACTGCA 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 232 gtggcgacatatgtgtgatatcttcttatactatctctcgtgtgatatattgg 311
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Db 235 ATGGCGCTTACACCTTGTGCTTCACCATGTGCTACACCATTAATTGCTTCTTGG 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 312 ctctgtctttgtgcatagctcttcatcatcatgtgcatc-----attaatgacccaga 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 CTTCAATGTGTGGCTCATTTATGTCCGAGGTGATGAGCACACGTGGGACCAAGA 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 366 catcacactctgtgtgacaaagctcatcttccacagggcctttgttccctaga 425
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 GTGCATCCCTTGTGTGAAGAACCTTAGTGGCTTTGTGTGCTTCTCTCTCATTTGA 434

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QY 426 gaccacacaccacatagatatggtatctgctgttactctgaagaatgtctgtgacct 485
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Db 435 GACACAAACACCACTTGGGTATGGCTTACAGTCAATTACAGAGAGTCCAGAGGGAT 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 486 gctcatgtgtatccctccagctcatcttaagtgtgcatcataaacttatactatgtgagc 545
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 CATTCCTCTTCTAGTGCAGAGCCATCTGGGCTCTATTGTGTAATGCTTCATATGGGTTG 554
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 546 tgccttggccaaatgagcaactgcctcgaagaagagacccacacttcttgaagtaact 605
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 CATGTTTATAAAGATCAGCCAGCCAAAGAGAGACAGACACCTCATGTTCTCCACAA 614
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 606 tgcactatagatgatgagatgtggaagcttgcctcatgtgtgagcatgtgtatttccg 665
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 TCGTGTATCTCATTCAGCGGATGAGAGCTATGCCATGTTCCGGGTAGGGGACTCCG 674
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 666 gccaaacccacgtgtgagaagagaaacagtlagagcccaacttcccgctataacgaagaag 725
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 675 AAATCCCATATGTGTGAGGCTTCATCCGCGCAAGCTTATCAAGTCCGGCAGACCA 734
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 726 tgaag-----gagatgacgaatgacatllaaagacccaatlagtcaa 770
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 735 AGAAGGGGAAATTCATCCCTTGACACAGACGACATTAACGTGGGCTTGCACATGTGTA 794
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QY 771 egaccaaatcatctctgttccaccggttaactatgttccaatgtgacatgagagccc 830
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 795 CGACCGCCTCTTCGTGTGTCTCCCTCTTCATCTCCATGATGATCAATGAGAAAGGCC 854
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 831 tctgtatgccccttgacggaagcagltgccaagaataactttagatttggtagact 890
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Db 855 TTTCTGGGAGATGCTCTCGGCTCAACTGAGCAGAGAGTTGAGGTGCTGTATCT 914
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 891 tatcatactgttgaatccactgagacatctccacatctagaagctcctatgttcccg 950
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 915 AGAAGGAGATGTAGAGAGCCACAGCATGACTTCCACAGACGACTCTTACATGATGATAC 974
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QY 951 araaatctctgtgggacataaggttaatatgtcttggtaaggttaaggaaglatlaca 1010
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Db 975 AGAGGTGCTCTGGGTGCACCGATTCACACACAGTCCCTTGGAAGAGGCTTCTATGTA 1034
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QY 1011 agtgaactgttcaagtttgaagaaggttgaagatatatgcccctttagagtgccaa 1070
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Db 1035 GGTGACTACACACTTTCACGACACCTATGAGCACACACACCCAGCTGTGTGCCAA 1094
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1071 gcaattgg 1078
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Db 1095 GGAGCTGG 1102

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RESULT 9
US-08-103-445-3
; Sequence 3, Application US/08103445
; Patent No. 5492825
GENERAL INFORMATION:
APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yun Nung
APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan
APPLICANT: Slesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco,
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,445
FILING DATE: 06-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619/MHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1889
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1827 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 59..1564
FEATURE:
NAME/KEY: misc.feature
LOCATION: 314..379
OTHER INFORMATION: /note= "Region encoding M1
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc.feature
LOCATION: 455..505
OTHER INFORMATION: /note= "Region encoding H5
OTHER INFORMATION: segment."
FEATURE:
NAME/KEY: misc.feature
LOCATION: 530..595
OTHER INFORMATION: /note= "Region encoding M2
OTHER INFORMATION: segment."
US-08-103-445-3

Query Match      11.1% Score 167.2; DB 1; Length 1827;
Best Local Similarity 50.9%; Pred. No. 2,7e-41;
Matches 486; Conservative 1; Mismatches 444; Indels 23; Gaps 3;

QY 148 cgattactccaaagatgagcagctgtaattctacttcaagcaatcttggagaatg 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 CGTTTCGTCGACGAAGACGGTCGTCATGTGCAGCAGCAACCTGGCAGCGAGACC 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 ggaagctatggtgtgacatctaccacactgtgtgacacaaagtggcgcatagttt 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 AGTGGCTACCTTTCCGACCTTTTACCTACCTGGTGATCTCAAGTGGCGTTGGAAC 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 268 gtgataatttcttatactatctctcgtgtgtgataatttgctctgtcttggctc 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 TTATATCTTACATCTACCTACACGTGGCTGCTTCATGAGGCTCATGTGGGGTG 370
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 328 atagccttcacatgagcagctatataatgatacag-----acatacaacctgtgtt 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 ATCCCTTATACCCGGGGGACCTTACAAACCCCATGTCGGCAACTACACTCCCTGTGTG 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 382 gacaagctccattcttccacaggggaccttgtcttccctgaagacccaacacacata 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 GCCAATGTCTTAACCTTCCCTTGCCTTCTTCTTCTTCAATCGAGACCGAGCCACATTC 490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 ggaatagttatcgctgttactgaagaatgtctgtgacgctgtcattgtatcctc 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 GGTATAGCTACCGCTACATCGACGAAGTGGCCCGAGGCGATCATCTTCTTCTTTC 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 cagtcacatcttaagtgtcatataataactcttatactatgagctgtcctgtggcaaatg 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 551 CAGTGCATCTTGGCTCATCGTGGAGCCCTTCTCATCGGCTGCATCATGTCATCAAGATG 610
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QY 562 gcaactgtcgaagaagagcccaaacatctgcgttccagctacttgcactatagatg 621
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DB 611 TCCAGGCCCAAAAGAGCGCGAGACCCCTCATGTTTACGAGCATGGCGTATTTCATG 670
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QY 622 agagatgggaagcttgcctcatgtgacatgtgtgatttgcggccaacacagtgta 681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 671 AGGACGGGAAACATCATCTCATGTGTCGGGTGGGCAACCTGCCAACACCCACATGTC 730
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QY 682 gaagaaagatgaagcccaactctccgcatalacagaagacagtgaaaggaatgacg 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 731 TCCGGCAGATCCGTCGACCTGCTCAAAATCT-CCGACAGACCTCGAGGATGATTC 789
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 742 atggcat-----ttaaagacctcaaatatgaatgaacgaaccaatcatcct 785
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 790 ACCCTTGACCACTTGACATGATGATGTTTATGATACAGGCGACATCACTTTTCT 849
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 786 ggtacccccggttaactatgtccatgaatgaacatgaagacccctctgttccttga 845
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 850 TGTGTCCCTCTCACCATTTGCCACGTGATGATGCCAAAGCCCTTTTATGACCTATC 909
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 846 ccgcaagcagtaagcgaagaatacttgaatlttgatgacattatctactgtgtga 905
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 910 CCAGCGAAGCATGCAAACTGAACAGTTGAGTGTGCTCATCTCGAAGGCAATCGTGA 969
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 906 ttccactggaacatctcaaccaatcagaagctcctatgttcccgaraaatctctcgtg 965
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 970 AACCAAGGATGATCTTCAAGCTCGAATCATATACCCGAAGATGAAGTTCTTTGGGG 1029
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 966 ccataggttaatgagcttgaagatgaaggaagattacaaagtgaactgtcttaca 1035
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1030 TCATCGTTTTCCTCTGAATTTCTTTAGAAAGAGATTTTAAAGTCATCTCCCA 1089
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1026 gttgaaggaagtgtggaagatatatgcccccttgcagtgatgcaagcatgga 1079
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1090 GTTCATGCAACCTTGAAGTCCACCCCTCCGTACAGTGTGAAGAGCAGAGA 1143
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```
RESULT 10
US-08-461-690B-3
Sequence 3, Application US/08461690B
Patent No. 5670335
GENERAL INFORMATION:
APPLICANT: Jan, Lily Y.
APPLICANT: Jan, Yuh Nung
APPLICANT: Kubo, Yoshihiro
APPLICANT: Reuveny, Eitan
APPLICANT: Slesinger, Paul A.
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,690B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,445
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58619-1/MHD/JPB
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1827 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 59..1561
FEATURE:
NAME/KEY: misc.feature
LOCATION: 314..379
OTHER INFORMATION: /note="region encoding M1
OTHER INFORMATION: segment.
FEATURE:
NAME/KEY: misc.feature
LOCATION: 455..505
OTHER INFORMATION: /note="region encoding H5
OTHER INFORMATION: segment.
FEATURE:
NAME/KEY: misc.feature
LOCATION: 530..595
US-08-461-690B-3

Query Match 11.1%; Score 167.2; DB 1; Length 1827;
Best Local Similarity 50.9%; Pred. No. 2.7e-41;
Matches 486; Conservative 1; Mismatches 444; Indels 23; Gaps 3;

148 cgaattacccaagaatgcaagctgtaattgtctactccaagaacatttttgagaatg 207
191 CGGTTGTGACAGAAACGGTGGTCAATGTGACAGACGGCAACCTGGGACGAGACC 250
208 ggaagataatgtgtgacacatctaccactctgtggaacaaagtggcgcatatgtt 267
251 AGTCGCTACCTTCCGACCTCTTCACTACCTGCTGATCTCAAGTGGCGCTTGAACCTC 310
268 ggaatatttcttactatattctctcgtgtgtgatatttggcctcgtcttggctc 327
311 TTATATCTTCAATCTCACTACCTGCTGCTTCAATGCGCTGATCTCAAGTGGCGCTT 370
328 atagccttcatcatggcgatcatatgaatgacacg-----acatacaccttggc 381
371 ATGCTTATACCGGGGCGACCTGACAAAGCCCATGTGCGCAACTACCTCCCTGTGTG 430
382 gacaacgtccattctctcacaggagccttcttctccctagagacccaacacacata 441
431 GCCAATGTCTATTAATCTCCCTCTGCTTCTTCTTCAATGACCGGACCCACCATC 490
442 ggaatagttatgctgtgttactgaagaatgttctgtgacgtgtccatgagtcctc 501
491 GGCTATGGCTACCGCTACACACCGAAGTGGCCCGAGGGGCATCATCTTTCTCTTTC 550
502 cagtcactcctaagttgacataaataactatatacttgagcctgtgagccaatg 561
551 CAGTCCATCTTGGCTCATCTGAGAGCTTCTCTCATCGGCTGCATGTTATCATCAATG 610
562 gcaactgctcgaagaagagcccaacatcgtttcagctacttctgacattatagatg 621
611 TCCAGCGCCAAAAGCGCGGAGACCTCATGTTTAGCAGCATGGGTTATTTCCATG 670
622 agagatgggaagcttctgctcctcatggtggcgcatgtgtatcttggccaacacagtgta 681
671 AGGAGACGGAACACTCTCATGTTCCGGGTGGGCAACCTGCGCAACACCAACATGCTC 736
682 gaaggaacagtttagagcccaactctcgcctatatacaagaagatgaaggagatgag 741
731 TCCGCGCATCTCGCTGCAAGCTGCTCAAAATCT-CGGCAGACACCTGAGGGTGAGTTTCT 789

QY 742 atggcat-----ttaagacctcaattagtcacagaccacatcatcct 785
DB 790 ACCCCCTTGACCACTTGAACGTGATGTAGTTTGTAGTACAGGGGCGAGATCAACTTTTCT 849
QY 786 ggtcaccggtaactatgttccatgaatattgacatgagaacccctctgtatgccttga 845
DB 850 TGTGTCCTCTCACCATTGTGCGACGTGATGTATGCAAAACCCCTTTATGACCTATC 909
QY 846 ccgaagaagtagccaagaataactlttgagatttggatcatatatactatg 905
DB 910 CCAGGACAGCATGCAAACTGAAACAGTTGAGGTGCTCATCTCTGAAGCGCATCGTGA 969
QY 906 tccactggaacatctcaccatctagaagctcctatgttcccgaaatctcctggg 965
DB 970 AACACAGGAGATGACTGTGCAAGCTGCAACATCATACACCGAAGATGAACTTTGGGG 1029
QY 966 ccaatgattatgattgtcttggaaagttaagagaagatlatcaaaagtgaactgtctaa 1025
DB 1030 TCATCGTTTTCCTGATATTTCTTAGAAGAGATTTCTTAAGTGATTAATCTCCCA 1089
QY 1026 gtttgaagaagtgtggaagatlatgcccccttltgcaagtgccaaagcaattgga 1079
DB 1090 GTTCATGCAACCTTGAAGTCCCAACCCCTCTGATAGTGTGAAGAGACAGGA 1143

RESULT 11
US-08-486-342-1
Sequence 1, Application US/08486342

GENERAL INFORMATION:
PATENT No. 5728535
APPLICANT: Lester, Henry A.
APPLICANT: Dascal, Nathan
APPLICANT: Lim, Nancy F.
APPLICANT: Schreimayer, Wolfgang
APPLICANT: Davidson, No. 5728535man
TITLE OF INVENTION: DNA Encoding Inward Rectifier,
TITLE OF INVENTION: G-Protein
TITLE OF INVENTION: Activated, Mammalian, Potassium KGA Channel and
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Flehr, Hohbach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,342
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-62319/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs

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: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 32..1534
: US-08-486-342-1

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Query Match      11.0%; Score 165.6; DB 1; Length 2070;
Best Local Similarity 50.8%; Pred. No. 9e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

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Db 164 CGGTTCTGGACAGAAAGCGGTGCAATGTGACAGCAGGCAACCTGGGACGAGAGACC 223

QY 208 ggaagctatgtggtgacatcttcaaccctctgtgagacaaagtgcgcatagttt 267
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Db 224 AGTGTCTACCTTTCCGACCTCTTCACTACCTGGTGATCTCAAGTGGCGTTGGAACCTC 283

QY 268 gtgataattcttattattattatctctgtgtgtgatatttgctgtcttctgtgctc 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 TTTATCTTCATCTCTACCTACCTACCGTGGCTGTCTCATGGCTCATGTGGTGGGTG 343

QY 328 atagccttcaatcagctgcatctataatgatccag-----acatcacacctgtgtt 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 ATGCTTATACCCGGGGGACCTTCAACAAACCCATGTCGGCAACTTACACTCCCTGTGTG 403

QY 382 gacaacgltcaatcttctacagagggccttltgtctccctagagaccacaacacata 441
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Db 404 GCCAATGTCTATACCTTCCCTCTGCTTCTTCTTCATCGAGACGAGCCACCATC 463

QY 442 ggaatgttatgcgtgtgttactggaagatgttctgtgcgtgtctcatgtgtatctctc 501
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 GGGCTATGGCTACCCCTCATCACCGACAAAGTCCCGAGGCGCATCATCTTTCTTTTC 523

QY 502 cagtcacatcttaagtcatcataataatcattatcattgtgagtgctgtggccaatgt 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CAGTCCATCTTGGCTCATCTGTGACGCTTCTCTCATGGCTGCATGTTATCAAGTGTG 583

QY 562 gcaactgtcgaagagagacaaacatttctgttcaacttcttcaactatagatgt 621
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TCCAGGCCCAAAAGGCGCGGAGAACCTCATGTTAGCGAGCATGGGTTATTTCATG 643

QY 622 agagatgtggaagcttcttccatgtgtgcgcatgtgtgtatttctggccaaccagtgta 681
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 AGGACGCGAAACTCTCATCTCATGTTCGGGTGGGCAACCTGCACACGACATGCTC 703

QY 682 gaagaaacaglttagagcccaacttctcgcctatcagaagaagtgagaagatgacg 741
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 TCCGCGAGATCCCTCTCAAGCTCTCAAACT-CCGACAGACCTTGAAGGTGATGTTCT 762

QY 742 atggcat-----ttaagaacctcaaatltagtcaagcaacaacatcatct 785
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 ACCCTTGACCAACTTGACATGTGATGAGTTTATTAGACAGGGCAGATCAACTTTTCT 822

QY 786 ggtacacccggttaactatgttccatgtaattgacacatgagagccctctgtatgccttga 845
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 823 TGTGTCCCTCTCTACCTTTGACGACGTGATGATGCCAAAACCCCTTTTATGACCTATG 882

QY 846 ccgcaaaagcagltagcaaaagataacttgagatttgtagcatlctatactgtgtga 905
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 883 CCAAGCAAGCATGCAAACTGATGACAGTTTCGAGGTGTCTCTCTGGAAGGACATGTGGA 942

QY 906 ttcacatggaacatctcaacaatctagaaatcctatgttcccgagaaatcttctcgtg 965
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 943 AACCAACAGGATGATGTCTCAAGCTCGAACATCATACACCAAGATGAAGTTTCTTGGGG 1002

QY 966 ccataagtttaatgattgtcttggaagtgagaagatlatcaaaatgtgaactcttaca 1025
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1003 TCATCGTTTTCCTCTTAATTTCTTTAGAAAGATTTCTTTAAAGTGCATTAATCTCCA 1062

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QY 1026 gtttgaagaaagtgtggaagatatagtccccccttgcagtgccaagcaattgga 1079
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1063 GTTCATGCAACCTTTGAAGTCCCAACCCCTTCCTGATAGTGTGAAGACGACGA 1116

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```

RESULT 12
US-08-473-092-1
: Sequence 1, Application US/08473092
: Patent No. 5734021
: GENERAL INFORMATION:
: APPLICANT: Lester, Henry A.
: APPLICANT: Dascal, Nathan
: APPLICANT: Lim, Nancy F.
: APPLICANT: Schreimayer, Wolfgang
: APPLICANT: Davidson, No. 5734021man
: TITLE OF INVENTION: DNA Encoding Inward Rectifier,
: TITLE OF INVENTION: G-Protein Activated, Mammalian,
: TITLE OF INVENTION: Potassium KGA Channel and Uses
: NUMBER OF SEQUENCES: 2

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Flehr, Hohbach, Test, Albritton
ADDRESSEE: 6 Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,092
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,426
REFERENCE/DOCKET NUMBER: A-62317/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

```

```

INFORMATION FOR SRO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

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```

NAME/KEY: CDS
LOCATION: 32..1534
US-08-473-092-1

```

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Query Match      11.0%; Score 165.6; DB 1; Length 2070;
Best Local Similarity 50.8%; Pred. No. 9e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

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QY 148 cgaattacttcaaaagatgagctgtaattgtaattctacttcaagccatttttgagaatg 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 CGGTTCTGGACAGAAAGCGGTGCAATGTGACAGCAGGCAACCTGGGACGAGAGACC 223

QY 208 ggaagctatgtggtgacatcttcaaccctctgtgagacaaagtgcgcatagttt 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 AGTGTCTACCTTTCCGACCTCTTCACTACCTGGTGATCTCAAGTGGCGTTGGAACCTC 283

```

OY	268	gtgatattcttattctattctattctctctgttggtgatattgagcctgtctttggcc	327
Db	284	TTTATCTTCACTCCCTACACTACACCGTGGCTCTTCAATGGCGTCAATGTGTGGTGT	343
OY	328	atagcccttcaatcagtcgagatctatattaaatgacag-----acataccacttgytt	381
Db	344	ATTCCTTATACCCGGGGGCGACCTGAACAAAGCCCATGTGGCAATCACTCCCTGTGTG	403
OY	382	gacaaagtccattcttctcaagaggcccttttgtcttcctctagaagcccaaccacata	441
Db	404	GCCAATGTCTATAACTTCCTCCCTCGCTTCCTTTCTTCAATCAAGACCGAAGCGACCAATC	463
OY	442	ggaatagttaacgtctgttacttgaagaaagtctctgtgacgttgatcattgtaaccc	501
Db	464	GGCTATGGCTACCGCTACATCAACCGAATAATGGCCGAGGGGATCATCTTTTCCCTTTC	523
OY	502	caatccatcttaagtctgcatcataataatccttaatcttggagctgccttgccaaatg	561
Db	524	CAGTCAATCCCTTGGCTCCATCGTGTGGAGCGCTTTCCTCATGGCTGCATATGTTCAATCAAGT	583
OY	562	gcaactgctcgaagaagagagcccaaaccttcgttttaagcttaacttgcacttaagtatg	621
Db	584	TCCACAGCCCAAAAAGCCGCGCGAGACCCCTATGTATGACGACATCGGTATTTCCATG	643
OY	622	agagatggaaagcttgcctcatgttggcgcatttggatatttcgcgcaaacacgttga	681
Db	644	AGGGACGGAAAACTCACTCTCATGTTCGGGGTGGGCAACTGGGCAACAGCCATGTGTC	703
OY	682	gaagaaacagtttagagcccaactctccgtatacagaagacagttgaaggagatgacg	741
Db	704	TCCCGCGAGATCCGCTCAAGCTCTCAATAATCT-CGCGACAGACACCTGAGGGTAGTTCCT	762
OY	742	atggcat-----ttaagaccctcaaatatgttaagaccacaatctcct	785
Db	763	ACCCCTTGACCACTTGAATCTGATGTAGGTATTAGTACAGGGGCGAGATCAACTTTTCT	822
OY	786	ggtcaccccggttaactatctgtccatgtgaatttgacatgagagccctctgtatcccttga	845
Db	823	TGTGTCCCTCTCAACATTTGCCACGTGATGATGATGCCAAAGGCCCTTTATATGACTTATC	882
OY	846	ccgcaagaagtagtgcacaaagataacttggagatttgggtacattatctatactactgtga	905
Db	883	CCAGCGAAGCATGTGAACCTGATMAAGTTCAGAGTGTGTCTCATCTGTGAAGGCATCTGTGA	942
OY	906	tttcaacttgaaacatctcaaccaatctagaagctcctatgtctcccgagaaatctctgggg	965
Db	943	AACCAACAGGATGTGACTTGTCTCAAGCTCAACAATCATACACCGAAGATGMAATTCTTTGGGG	1000
OY	966	ccataagtttaatgatgtctctggaagttlaagagaaatctatacaagatgtaactgtctaa	1021
Db	1003	TCATCTGTTTTTCCCTGTAAATTTCTTTAGAAAGATGATCTTTTAAAGTGCATTATCTCCA	1060
OY	1026	gtttgaagaaagatgttggaagataatgccccctttggaagtgcgaagaatgtga	1079
Db	1063	GTTCCATCAACCTTTTGAAGTCCCAACCCCTCCGCTAGAGTGTGAAGAAGCAGAGA	1116

RESULT 13
US-08-614-801A-1
: Sequence 1, Application US/08614801A
: Patent No. 5744324
: GENERAL INFORMATION:
: APPLICANT: Lester, Henry A.
: APPLICANT: Davidson, No. 5744324man
: APPLICANT: Kofuji, Paulo
: TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
: TITLE OF INVENTION: MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fleh, Hohbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
:

```

STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,801A
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Treccartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-63098/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2070 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 32..1534
US-08-614-801A-1

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Query Match	Similarity	11.0%	Score 165.6	DB 1	Length 2070
Best Local	Similarity	50.8%	Pred. Num. 9e-41		
Matches	485	Conservative	1	Mismatches 445	Indels 23
					Gaps 3
QY	148	cgattacttcaacaaagatgacgcgtgtaatgctacttcaagacacatttttggagatg	207		
Db	164	CGGTTGCGGACAAAGACGGTGGGTCATGTGACACGACGGCACTGGGACGGAC	223		
QY	208	ggaagctatgtygttgtaacatcttcaaccactcttgygacaccaaigtgcgcatatgtt	267		
Db	224	AGTCGCTACCTTTCCGACCTCTTCACTACCCGTGGTGATCTCAAGGGGCTTGAACCTC	283		
QY	268	ggtgatatttcttcttctataatctctgtygttgatatatttggcgtgtctttggc	327		
Db	284	TTTATCTTATCTTACCTACCTACCTACCGGTGGCTCTTATATGGCTTCATGTGGTG	343		
QY	328	atagccttcaatcaltgagcgatcatlataatgatacag-----acatacaccttgyt	381		
Db	344	ATCGCTTATACCCGGGGGCGACCTGAACAAAGCCATGTGGGCACTACACTCCCTGTGG	403		
QY	382	gacacgctccatctcttctcaaggggccttttgtctctccctagaagacccaacacacata	441		
Db	404	GCCATGTCTTAACTTCCCTCGCTCTCTTTCCTTATCGAGACGAGGCCACATTC	463		
QY	442	ggatatgttatcgctgtgttactgaagaagtctctgtygcgtgtctatgtytatccct	501		
Db	464	GGCTTATGGCTACCGTACATCAACGCAAGTCCCGGAGGGATCATCTTTTCTTTTC	523		
QY	502	cagtcatacttaagtgcatacctaataacttataacttatactgagagtcgctctggccaatg	561		
Db	524	CAGTCATCTTGGCTCCATCGTGGAGCTTTCCTCATGGCTGCATGTTCATCAAGATG	583		
QY	562	gaaactgtcgaagaagaaacccaacatctgtttcagctacttgcacttataagatga	621		
Db	584	TCCCAAGCCCAAAAGACGGCGGACGACGCCATCATGTTTAGGAGAGATGGCTTATTTCATG	643		
QY	622	agagatgggaagcttgcctcatatgtygcgcatgtygatttctcgccaacaacgtygta	681		

DB 644 AGGAGGAGAACTCACTCATGTTCCGGGTGGGCAACCTGCGCAACGCCACATGTC 703
QY 682 gaaggaacagltgagcccaattctccgtatatacagaacagcgtgaaggaagatgag 741
DB 704 TCCGCGCAGATCCGTCGCAAGCTGCTCAAAATCT-CCGCAACACATGAGGGTGTCT 762
QY 742 atggcat-----ttaagacctcaattagtcacagccaatcatcct 785
DB 763 ACCCTTGACCACTTGAACTGATGATGTTTAGTACAGGGGAGATCACTTTTCT 822
QY 786 ggtcaccggtaactattgtccataaattgacccatgagaccctctgtatcccttga 845
DB 823 TGTGTCCTCCCTCACCATTGTCACGTCGATGCGCAAAAGCCCTTTATACCTATC 882
QY 846 ccgcaaaagcagtagccaagaataacttggatgttggtagcatlatacatalctgtga 905
DB 883 CCAGCGAAGCATCAAACTGACATGATCGAGTGTGCTGATCCTGGAAGCATCTGGA 942
QY 906 ttccactgagacatctcaaccaatctagaagctcctatgttcccgaraaattctctgg 965
DB 943 AACCAAGAGGATGACTTGTCAAGCTCGAATATACCGAAGATGATGATCTTTGGG 1002
QY 966 ccaatggttaatgagtcttggaaagltgaaggaagltatacaagtgtaactgttaca 1025
DB 1003 TCATGCTTTTTCCTGTAATTTCTTTAGAAAGATCTTTAAAGTCATTAACCTCCA 1062
QY 1026 gtttgaagaagtgtagaatatatacgcccttggcagtgccaagaattga 1079
DB 1063 GTTCATGCAACCTTGAAGTCCCAACCCCTCCGTACAGTGAAGAGCAGGA 1116

RESULT 14
US-08-066-371-1

Sequence 1, Application US/08066371
Patent No. 5747278
GENERAL INFORMATION:
APPLICANT: Lester, Henry A. et al.
TITLE OF INVENTION: ISOLATION OF A DNA ENCODING A
TITLE OF INVENTION: G-PROTEIN ACTIVATED, MAMMALIAN, POTASSIUM
TITLE OF INVENTION: KGA CHANNEL AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,371
FILING DATE: 19930521
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43717/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2076 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 32..1534
US-08-066-371-1

Query Match 11.0%; Score 165.6; DB 1; Length 2076;
Best Local Similarity 50.8%; Pred. No. 9, 1e-41;
Matches 485; Conservative 1; Mismatches 445; Indels 23; Gaps 3;

QY 148 cgattacttacaagaatgagcagctglaatgttacttcaagaacatltttgagaatg 207
DB 164 CGGTTGGTGACCAAGACGGTCGTCGAATGTGCACACGCGCAACCTGGGACAGACC 223
QY 208 ggaagctatgtgtgaactctcacacactgtgtgagacccaagtgagccatagtt 267
DB 224 AGTCGCTACTTTCGACCTCTTCACTTACCTGTGTGATCTCAAGTGGCTTGAACCTC 283
QY 268 gtgatatcttcttatacttatactctcgtgtgtatattgtcctgtcttggctc 327
DB 284 TTATCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 343
QY 328 atagccttcaatcagtgagcagctataatgatccag-----acatcacactgtgt 381
DB 344 ATCGCTTATACCGGGGCGACCTGAACAAAGCCCATGTGCGCAACTCTCTGTG 403
QY 382 gacaagctcatcttctcaagagggccttltgttcccttaagaagcccaaccacata 441
DB 404 GCGAATGTCTAATCTTCCCTCTGCTCTTCTTCTTCACTGAGACCGAGGCGACCATC 463
QY 442 ggaatggtatcgtgtgttactgaagaatgttctgtgctgtgtcagtgatcctc 501
DB 464 GGTATGAGTACCGGTACATCACTCACTCACTCACTCACTCACTCACTCACTCACT 523
QY 502 cagtcacatcttaagtgatcacaataatcttatacttgaagctgtcctgtgccaagt 561
DB 524 CAGTCCATCTTGGCTCCATCTGTCGACGGCTTCTCATCGGCTGATGTTCACTCAAGAT 583
QY 562 gcaacgtctgaagaagagcccaaccatctgttgaagcttcttgaacttgcactatagtg 621
DB 584 TCCAGCGCCAAAGAGCGCGCGAGACCTCATGTTAGGAGCATCGGTTATTTCCATG 643
QY 622 agaatggaagaagcttgcctatgtgctgcatgtgtatcttgcgccaacacagtgta 681
DB 644 AGGAGGAGAACTCACTCATGTTCCGGGTGGGCAACCTGCGCAACGCCACATGTC 703
QY 682 gaaagaaagltagagcccaattctccgtatatacagaagaagtgaaaggaatgag 741
DB 704 TCCGCGCAGATCCGTCGCAAGCTGCTCAAAATCT-CCGCAACACATGAGGGTGTCT 762
QY 742 atggcat-----ttaagacctcaattagtcacagccaatcatcct 785
DB 763 ACCCTTGACCACTTGAACTGATGATGTTTAGTACAGGGGAGATCACTTTTCT 822
QY 786 ggtcaccggtaactattgtccataaattgacccatgagaccctctgtatcccttga 845
DB 823 TGTGTCCTCCCTCACCATTGTCACGTCGATGCGCAAAAGCCCTTTATACCTATC 882
QY 846 ccgcaaaagcagtagccaagaataacttggatgttggtagcatlatacatalctgtga 905
DB 883 CCAGCGAAGCATCAAACTGACATGATCGAGTGTGCTGATCCTGGAAGCATCTGGA 942
QY 906 ttccactgagacatctcaaccaatctagaagctcctatgttcccgaraaattctctgg 965
DB 943 AACCAAGAGGATGACTTGTCAAGCTCGAATATACCGAAGATGATGATCTTTGGG 1002
QY 966 ccaatggttaatgagtcttggaaagltgaaggaagltatacaagtgtaactgttaca 1025
DB 1003 TCATGCTTTTTCCTGTAATTTCTTTAGAAAGATCTTTAAAGTCATTAACCTCCA 1062
QY 1026 gtttgaagaagtgtagaatatatacgcccttggcagtgccaagaattga 1079
DB 1063 GTTCATGCAACCTTGAAGTCCCAACCCCTCCGTACAGTGAAGAGCAGGA 1116

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